

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 17, 2002, 23:52:22 ; Search time 1381.58 Seconds

(without alignments)
9910.869 Million cell updates/sec

Title: US-09-358-321C-31

Perfect score: 830
1 cctagaatgtaagcgctat.....ctgaattagtaagcgccgcg 830

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Listing first 45 summaries

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GenBml:
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2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
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36: em.htg.other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	502.4	60.5	759	12	SCO250763	AJ250763 Mus muscu
2	501.2	60.4	1637	6	AX006750	AX006750 Sequence
3	499	60.1	753	6	AX003768	AX003768 Sequence
4	499	60.1	753	6	AX003776	AX003776 Sequence
5	482.6	58.1	864	12	XXU31739	U31739 Single chai
6	476.6	57.4	732	12	XXU44796	U44796 Synthetic c
7	476	57.3	792	12	AP276797	AP276797 Synthetic
8	411.6	49.6	768	6	AS7272	AS7272 Sequence 4
9	407.6	49.1	749	6	AS9386	AS9386 Sequence 36
10	403.2	48.8	1511	6	AS9381	AS9381 Sequence 31
11	404.6	48.7	729	12	AC013152	AU131532 Synthetic
12	397.2	47.9	1101	6	AB2599	AB2599 Sequence 1
13	397.2	47.9	1103	6	AB2600	AB2600 Sequence 2
14	392.8	47.3	795	10	KMSCV25	270662 Artificial
15	389.6	46.9	738	10	AF141321	AF141321 Mus muscu
16	381.6	46.0	925	6	E30617	E30617 Antibody an
17	380.4	45.8	772	6	AR085460	AR085460 Sequence
18	380.4	45.8	772	6	AR088866	AR088866 Sequence
19	380.4	45.8	772	6	136723	136723 Sequence 33
20	380.4	45.8	772	12	S57990	S57990 B3(PV)-PE40
21	380.4	45.8	912	12	AB030249	AB030249 Synthetic
22	370	44.6	747	6	A33046	A33046 Anti-oxazol
23	369.4	44.5	720	12	AP059737	AP059737 Synthetic
24	368.8	44.4	918	6	E31219	E31219 Device for
25	368.8	44.4	804	6	A95255	A95255 Sequence 1
26	367.8	44.3	747	6	AX100176	AX100176 Sequence
27	367.2	44.2	879	6	E16309	E16309 DNA encodin
28	365	44.0	774	12	SCU65537	U65537 Synthetic M
29	364.6	43.9	825	12	SCU65536	U65536 Synthetic M
30	364.2	43.9	726	6	AX146641	AX146641 Sequence
31	362.4	43.7	864	6	AB3227	AB3227 Sequence 47
32	355.8	42.9	810	10	NMU62527	U62527 Mus muscu
33	354.2	42.7	3970	12	ASY14585	Y14585 Artificial
34	352.6	42.5	4363	12	SCFV18290	Y18290 Expression
35	352.6	42.5	4864	12	ASY14584	Y14584 Artificial
36	352.4	42.5	747	10	MMVHVKFC	229480 M.musculus
37	350.2	42.2	3991	12	ASY12778	Y12778 Artificial
38	348.2	42.0	738	6	AR085459	AR085459 Sequence
39	348.2	42.0	738	6	AR088865	AR088865 Sequence
40	348.2	42.0	738	6	136722	136722 Sequence 31
41	347.4	41.9	1653	6	AX011208	AX011208 Sequence
42	347.4	41.9	1698	6	AX011206	AX011206 Sequence
43	347.4	41.9	2010	6	AR112914	AR112914 Sequence
44	344	41.4	4354	12	ASY14583	Y14583 Artificial
45	343.6	41.4	744	12	AF402256	AF402256 Synthetic

ALIGNMENTS

RESULT 1	SCO250763	759 bp	mus musculus synthetic construct for anti-guinea pig C5 scfv	SYN	11-MAY-2000
LOCUS	SCO250763		antibody, clone D10.		
DEFINITION	mus musculus synthetic construct for anti-guinea pig C5 scfv				
ACCESSION	AJ250763				
VERSION	AJ250763.1	GI:6272278			
KEYWORDS	antibody; heavy chain; immunoglobulin superfamily; light chain; scfv; variable region.				
SOURCE	Scfv: variable region.				
ORGANISM	synthetic construct.				
REFERENCE	1 (bases 1 to 759)				
AUTHORS	Link,C., Hawlicsch,H., Meyer zu Vilsendorf,A., Gylteruez,S., Nagel,E. and Koehn,U.				
TITLE	Selection of phage-displayed anti-guinea pig C5 or C3a antibodies and their application in xenotransplantation				
JOURNAL	Mol. Immunol. 38, 1235-1247 (1999)				
REFERENCE	2 (bases 1 to 759)				
AUTHORS	Link,C.				

[illegible]

Db	121	AGACTGCGAAGAGCCCTTACGTGAGATTGGAGAGAGCTTTATCTCAGAAATGGTAAATGCTTAC	180
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Qy	691	agagtggaagctbaagatctggaattattctgcctcctaagtaacaatgttcggtac	750
Db	661	AGAGTGAAGGCTAGGATCTGGAGATTTATTTCGTCTCAAGTACATGTTCCGTAC	720
Qy	751	acgttcggaaggggagccaaagctgaaataaa	783
Db	721	ACGTTGCGAAGGGGAGCAACGTTGAGATCAAA	753
RESULT 4			
AX003776	753 bp	DNA	PAT 24-AUG-2000
LOCUS	Sequence 70	from Patent WO92-5818.	
DEFINITION	AX003776		
ACCESSION	AX003776.1	GI:9927575	
VERSION			
KEYWORDS			
SOURCE	Mus sp.		
ORGANISM	Mus sp.		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 753)		
AUTHORS	Kufer, P. and Raum T.		
TITLE	Method of identifying binding site domains that retain the capacity		
JOURNAL	of binding to an epitope		
	Patent: WO 92/5818-A 70 27-MAY-1999;		
FEATURES	KUFER PETER (DE); RAUM TOBIAS (DE)		
	Location/Qualifiers		
source	1..753		
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Query Match	60.1%; Score 499; DB 6; Length 753;		
Best Local Similarity	81.7%; Pred. No. 1,6e-140;		
Matches 615; Conservative	0; Mismatches 105; Indels 33; Gaps 2;		
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Db 466 GGATCGAGTGTGATGACCAACTCCACTCCCTGCTATACAGTCTTGAGATCAA 525
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Db 526 GCCCTCATCTCTTGTATATCTAGTCAGAGCATTTGACATGTAAGGAACCTATCA 585
QY 562 catgtgacctgcagaaagccagctctccaaagctcctgatactacaagtctcaac 621
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Db 706 AAGATCAACAGAGTGCAGGCTGAGGATCTGGAGTTTATTACGCTTCAAGTTTCAACT 765
QY 742 gtcccgtaacagcttcggaaggaggaccagctcgaataaa-----agaagaa 789
Db 766 CTTCCTGACACAGCTTCGAGAGGGGAGCCACCAAGCTGGAATCAACGSGGCGCCAGAACAA 825
QY 790 aactcatctcagaagaagagatctgaat 816
Db 826 AAACCTCATCTCAGAGAGGATCTGAAAT 852

RESULT 6
LOCUS XXU44796 732 bp mRNA SYN 03-FEB-1996
DEFINITION Synthetic construct single-chain anti-acetylaminofluorene antibody
mRNA, from PCR amplified mouse VH and VL regions, partial cds.
ACCESSION U44796
VERSION U44796.1 GI:1177222
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 732).
AUTHORS Guesdon, J.-L. and Muller, B.H.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-1996) Jean-Luc Guesdon, Institut Pasteur, 28, rue
du Docteur Roux, Paris, 75015, France
FEATURES
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1..732
Location/Qualifiers
1..732
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/note="heavy chain V(D)J region"
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/note="synthetic primer"
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/note="single-chain antibody"
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Best Local Similarity 80.6%; Pred No. 1e-133;
Matches 586; Conservative 0; Mismatches 129; Indels 12; Gaps 2;

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Db 3 GGTCACTGCTCAGCAGAGCTGGGCTGAAGCTGGCAAACTGGGGCTCAGTGAATGTC 62
QY 129 ctgaaagcttggtggtcctaacacatttactgactatgaataaacctgggtgagcagacc 188
Db 63 CTGAAGGCTTCTGGCTACACCTTACTACTGATGCACTGGATGATGAACAGAGGC 122
QY 189 tgtcatalgacctgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaa 248
Db 123 TGACAGAGGCTGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 182
QY 249 tcgaagttcaagagacagagccatgagctgagctgagctgagctgagctgagct 308
Db 183 TCAGAACTTCAAGGACAAAGGCTGACTGACGCAAAATCTCCAGACAGCTTACAT 242
QY 309 ggaagctcgcagagctgacatctgaagctcgtgcgtctactactatacaag----- 359
Db 243 GCAACTAGCAGAGCTGACATCTGACATCTGACATCTGACATCTGACATCTGACATCT 302
QY 360 atggtctgagagactggtggtccaaaggagctgtgactgtctctgca---gaggttaatc 416
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QY 417 ctcaagatctggtctccgaatccaaaccggagatgtgtgatgagaccacaaccacttc 476
Db 363 AGGCGAGGAGTGGCTCTGCGGTGGCGATCGACATCGACATCGACATCGACATCTCTC 422
QY 477 cctgctcgtcagctctgtgagatcaagcctccatctctgcaatctagtcagagccttt 536
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Db 663 TTATTTCGCTCCAACTTACACATGTCCTGACAGTTGCGAGGGGAGCAACTGGA 722
QY 777 aataaa 783
Db 723 GCTGAAA 729

RESULT 7
LOCUS AF276797 792 bp mRNA SYN 02-JUN-2001
DEFINITION Synthetic construct anti-sperm scFv antibody RASA mRNA, partial
cds.
ACCESSION AF276797
VERSION AF276797.1 GI:14279759
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 792)
AUTHORS Norton, E.J., Diekmann, A.B., Westbrook, A., Flickinger, C.J. and
Herr, J.C.
TITLE RASA, An Anti-Sperm ScFv Directed Against the Sperm Glycoform of

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Db	427	TTGATGACCCAAACTCCACTCACTTTGTGGTTACCATTTGGACACCAAGCCTTCATCT	486
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Db	667	GTGAGAGCTGAGATTGGATTTGGAGATTATATCTCTGGCAAGGTACACATTCCTCCCTAC	726
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LOCUS	A59386	749 bp	DNA
DEFINITION	Sequence 36 from Patent WO9704092.		PAT
ACCESSION	A59386		
VERSION	A59386.1	GI:3714722	
KEYWORDS			
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 749)		
AUTHORS	Conseiller, E. and Bracco, L.		
TITLE	P53 PROTEIN VARIANTS AND THERAPEUTICAL USES THEREOF		
JOURNAL	Patent: WO 9704092-A 36 06-FEB-1997;		
COMMENT	RHONE-POULENC RORER SA (FR)		
FEATURES	Other publication FR 2736915 970124.		
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Db	61	GTCAGATTGCTCCGACACAGCTTCTGGCTTCAACATTAAAGACTCTATATGACATGGGTG	120
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QY	298	acacacctcaagtgagttccgcagcgccgaatcttgaaagactctgcgcgtctattactataca	357
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QY	358	agac-----ggttcagagacttgaggccaaggaactcgttcactgctctcgcagag	408

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QY	706	gattcggagattatattctcgtctcaaaagtaacacatgttccgtacaagttcggagaggg	765
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Db	721	ACCAAGCTGGAGCTGAAA	738
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LOCUS	A59381	1611 bp	DNA
DEFINITION	Sequence 31 from Patent WO9704092.		
ACCESSION	A59381		06-MAR-1998
VERSION	A59381.1	GI:3714713	
KEYWORDS			
SOURCE	unidentified.		
ORGANISM	unidentified.		
REFERENCE	1 (bases 1 to 1611)		
AUTHORS	Conseiller/E. and Bracco/L.		
TITLE	P53 PROTEIN VARIANTS AND THERAPEUTICAL USES THEREOF		
JOURNAL	Patent: WO 9704092-A 31 06-FEB-1997;		
COMMENT	PHONE: POULENC ROBER SA (FR)		
FEATURES	Other publication FR 2736915 970124.		
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Best Local Similarity	74.1%;	Pred.No. 5.7e-112;	

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OY	657	tgatcagagacagattcaactcaagaatcagagagtgtaggctcgagatctggagt	716	
Db	603	TGGATTCAGGGACAGATTTCACACTTTAAATCACAGAGGTGAGAGCTGAGATTGGGAGT	662	
OY	717	ttattctgcttccaagtaacacatctctgcagacccttcggagggagagcaagctgga	776	
Db	663	TTATTATTGCTGGCAAGGTACACATCTCTCCGCTTACGTTCCGTTGCTGCACCAAGCTGGA	722	
OY	777	ataaaa	783	
Db	723	AATTAA	729	
RESULT	12			
LOCUS	A82599	1101 bp	DNA	PAT
DEFINITION	Sequence 1 from Patent WO9854312.			21-JAN-2000
ACCESSION	A82599			
VERSION	A82599.1	GI:6732343		
KEYWORDS	unidentified.			
SOURCE	unclassified.			
ORGANISM	unclassified.			
REFERENCE	1 (bases 1 to 1101)			
AUTHORS	He,M. and Tauszig,M.J.			
TITLE	RIBOSOME COMPLEXES AS SELECTION PARTICLES FOR IN VITRO DISPLAY AND EVOLUTION OF PROTEINS			
JOURNAL	Patent: WO 9854312-A.1 03-DEC-1998; BABRAHAM INST (GB); HE MINGYUE (GB)			
FEATURES	BABRAHAM INST (GB); HE MINGYUE (GB)			
Source	Location/Qualifiers			
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Best Local Similarity	73.2%;	Pred. No. 1.5e-109;		
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			Gaps	2
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Db	111			
Db	36	GSAGGTCAAROTCGASAGAGTCWGGACTTAGCTGGAAGAAGCCTGGAGAGACAGTCAGAT	95	
OY	126	gtcctcgaaggcttcgggcttacacatttactctgactatgaaataacacgtggtgaggcagac	185	
Db	96	CTCCGCAAGGCTTCTGGGTATCCCTTCAAAAACATATGAGATGAACTGGGTGAAGGAGGC	155	
OY	186	acctgtgatgacctggaatggaatggaactatgatlucctgaaccttggttactgcta	245	
Db	156	TCCAGAGAAAGATTTAAAGTGAATGGCTGCGATGAACATCTACATGCGGAGCCAACATA	215	
OY	246	caatcagaagtccaaggacaagoccatagtgactgtagaacaalccctccagacacagcta	305	
Db	216	TGTTGATGACTTCAAAGGAGCGTTTGCTCTCTCTTTGGGAACCTCTGCACACACTGCTTA	275	

QY	306	caatgagctccgaagcctgacatctgaaacatcttcgcgtcttactatacaaga-----	360
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QY	361	-----tggtttaggactggggccaaggagactctgtaactgtctctgcaga	407
Db	336	CTAGCTCAACTGAGACTGAGTGTCTGCGGGCCACAGGACACAGGTCAACCGTCTCTAGC	395
QY	408	gggtaaatccctcaggaatctggtctccgaatccaaccggggatgttgtatgaccccaaa	467
Db	396	CAAAACACACACCCCATCTGTATC-----CACTGGCCAGAGCTCGATGAGACCCAGAT	449
QY	468	cccaactccctgcctcagctcgtcttgagatcaagcccacatccctctgcagatctga	527
Db	450	TCCACTCTCCCTGCTGTCTCAATTTTGAGATCAACCCCTCACTCTTTCAGATCTATCA	509
QY	528	gaagcctttcaacaagtaatgaaatcaaccattacattgtaactgtcagaagccaggcca	587
Db	510	GAGCGTGTACACAGTATGAAACACACCTATTACATTGATGATACCTGCAGAGCCAGGCCA	569
QY	588	gtcccaaaagctccctgatacacaagaattccaacagattctctggggtcccaagcagtt	647
Db	570	GTCCTCAAAGCTCCTATCTACAAATTTCCACAGGATTTTATGGGGTCCAGACAGTT	629
QY	648	caatggcagatgatacaggagacagattccaactcaagatcagcagaagtgaagctgaga	707
Db	630	CAGTGCACATGGAGATCAGGACAGACATTTCACTCAAGATCAAGATGACAGAGTGAAGC	689
QY	708	tcctggagttattatctgcctcctcaagatcacatgttccagacagttccgaaggaggac	767
Db	690	TCTGGAGATTATTATTTCTGCTCTAAGATTCAATATTCTTCGACAGTTCCGATGAGGAC	749
QY	768	caagctggaataaaaa	783
Db	750	CAAGCTGGAATTCAAA	765
RESULT	13		
LOCUS	A82600	1103 bp	DNA
DEFINITION	Sequence 2 from Patent WO954312.		
ACCESSION	A82600		
VERSION	A82600.1	GI:6732344	
KEYWORDS			
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 1103)		
AUTHORS	He, M. and Tauszig, M. J.		
TITLE	RIEOSOME COMPLEXES AS SELECTION PARTICLES FOR IN VITRO DISPLAY AND		
JOURNAL	EVOLUTION OF PROTEINS		
FEATURES	Patent: WO 9854313-A 2 03-DEC-1998;		
	BAHRAHM INST (GB); HE MINQUE (GB)		
Source	Location/Qualifiers		
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	/db_xref="taxon:32644"		
BASE COUNT	309 a	281 c	263 g
ORIGIN	245 t	5 others	
Query Match	47.9%	Score 397.2;	DB 6;
Best Local Similarity	73.2%;	Pred. No. 1.5e-109;	Length 1103;
Matches 539;	Conservative	5;	Mismatches 168;
		Indels	24;
		Gaps	2
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Db	38	GSAGGTCAKARTCGAGSAGTCGACCTAGAGTGAAGAGCCTGGAGAGACAGCTCAAGAT	97
QY	126	gtcctgcaaggcttcgggtacacatttactgactatgaataacacatggtggtgagcgac	185
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[illegible][illegible]

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 17, 2002, 23:54:57 ; Search time 110.25 Seconds
(without alignments)
6454.240 Million cell updates/sec

Title: US-09-358-321c-31

Perfect score: 830
Sequence: 1 tctagatgtgaagcgctat.....ctgaattagtaagcgcgcg 830

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	830	100.0	830	21	AA61047
2	528	63.6	828	21	AA61047
3	526.4	63.4	828	21	AA61047
4	521.4	62.8	819	21	AA61047
5	519.8	62.6	819	21	AA61047
6	510.8	61.5	876	19	AAV10390
7	501.2	60.4	1637	21	AA688358
8	499	60.1	753	20	AA677245
9	499	60.1	753	20	AA677241
10	476	57.3	753	22	AA670025
11	476	57.3	792	22	AA660021

Result No.	Score	Query Match	Length	DB ID	Description
12	447	53.9	459	21	AA61045
13	444	53.5	792	22	AA660022
14	443.4	53.4	786	22	AA660026
15	423.4	51.0	438	21	AA61046
16	419.4	50.5	1135	20	AA658936
17	415	50.0	1047	20	AA621156
18	415	50.0	1086	20	AA621158
19	411.6	49.6	768	17	AA648000
20	409.4	49.3	729	19	AA636236
21	408.2	49.2	753	21	AA661064
22	407.6	49.1	749	18	AA686234
23	405.2	48.8	1611	18	AA686234
24	401.4	48.4	726	20	AA686942
25	401.4	48.4	726	20	AA686943
26	397.2	47.9	1101	20	AA684663
27	397.2	47.9	1101	20	AA684663
28	393	47.3	782	16	AA686755
29	381.6	46.0	778	14	AA635955
30	381.6	46.0	925	21	AA658664
31	381.6	46.0	925	21	AA644206
32	380.4	45.8	772	14	AA635954
33	380.4	45.8	772	14	AA635954
34	368.8	44.4	879	19	AA631120
35	368.8	44.4	909	21	AA644235
36	368.8	44.4	918	21	AA644236
37	368.4	44.4	804	20	AA630724
38	367.8	44.3	747	22	AA630724
39	365.2	44.0	747	13	AA621098
40	364.2	43.9	726	22	AA624008
41	362.4	43.7	864	20	AA672072
42	361	43.5	723	19	AA610375
43	361	42.2	699	17	AA616700
44	350	42.2	1094	21	AA660982
45	347.4	41.9	1653	21	AA643432

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
1	830	100.0	830	21	AA61047
2	528	63.6	828	21	AA61047
3	526.4	63.4	828	21	AA61047
4	521.4	62.8	819	21	AA61047
5	519.8	62.6	819	21	AA61047
6	510.8	61.5	876	19	AAV10390
7	501.2	60.4	1637	21	AA688358
8	499	60.1	753	20	AA677245
9	499	60.1	753	20	AA677241
10	476	57.3	753	22	AA670025
11	476	57.3	792	22	AA660021

QY 106 cctgggcttcaagtacgctctcctgaaggtctcggtggtacacattactactatga 165
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 Db 751 acgttcgagagggggagacacagctcgaataataaagaagaanaa 792
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RESULT 3

AAA92443
 ID AAA92443 standard; DNA: 828 BP.

AAA92443:

15-JAN-2001 (first entry)

Plasmid pscm2 MAB12-scfv nucleotide sequence SEQ ID NO:24.

Monoclonal antibody; MAB12, IAP, integrin associated protein;

single stranded Fv; apoptosis; blood disease; leukaemia;

cytostatic; ds.

Mus sp.

WO200053634-A1.

14-SEP-2000.

10-MAR-2000; 2000WO-JP01458.

99JP-0063557.

XX (CHUGAI) CHUGAI SEIYAKU KK.
 PA Fukushima N, Uno S;
 XX
 PI
 XX
 DR WPI: 2000-587428/55.
 DR P-PSDB: AAB23819.
 XX
 PT Single stranded Fv antibody fragment inducing apoptosis in nucleated
 PT blood cells having integrin associated protein for treatment of
 PS leukemia
 PS Example 5; Page 64-66; 73pp; Japanese.
 XX
 CC The present invention describes a polypeptide containing the variable
 CC region of the light chain of a monoclonal antibody, which induces
 CC apoptosis in nucleated blood cells having integrin associate protein
 CC (IAP). Also described are: (1) DNA encoding the novel polypeptide;
 CC (2) animal or microbial cells expressing the DNA of (1); and (3) agents
 CC for the treatment of blood disorders which contain the polypeptide.
 CC The polypeptide can be used in the treatment of blood disorders such
 CC as leukemia. The present sequence encodes the protein sequence from
 CC pscm2 MAB12-scfv, which is used in an example from the present
 CC invention.
 XX
 SQ Sequence 828 BP; 210 A; 199 C; 219 G; 200 T; 0 other;
 Query Match 63.4%; Score 526.4; DB 21; Length 828;
 Best Local Similarity 82.8%; Pred. No. 2,4e-139;
 Matches 631; Conservative 0; Mismatches 116; Indels 15; Gaps 2;
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 Db 46 gctggccaacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 105
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 Db 346 tattactatacaagatg-----ttgagagactggggccaaaggagctctgttc 393
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Db      |||||
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Db      |||||
706 agaattgagagctgagagctgagatttattctgctccaagtaacatgtccgac 765
QY      751 agcttcgagaggggagacacagctggaataaagaagaanaa 792
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RESULT 4

AAA92442 standard; DNA: 819 BP.

AAA92442;

15-JAN-2001 (first entry)

Plasmid pCHOM1 MABL1-scrV nucleotide sequence SEQ ID NO:23.

Monoclonal antibody; MABL; IAP; integrin associated protein;
single stranded Fv; apoptosis; blood disease; leukemia;
cytostatic; ds.

Mus sp.

WO200053634-A1.

14-SEP-2000.

10-MAR-2000; 2000WO-JP01458.

10-MAR-1999; 99JP-0063557.

(CHUS) CHUGAI SEIYAKU KK.

Fukushima N, Uno S;

WPI: 2000-587428/55.

P-PSDB: AAB23818.

Single stranded Fv antibody fragment inducing apoptosis in nucleated
blood cells having integrin associated protein for treatment of
leukemia -
Example 5; Page 62-64; 73pp; Japanese.

The present invention describes a polypeptide containing the variable
region of the light chain of a monoclonal antibody, which induces
apoptosis in nucleated blood cells having integrin associated protein
(IAP). Also described are: (1) DNA encoding the novel polypeptide;
(2) animal or microbial cells expressing the DNA of (1); and (3) agents
for the treatment of blood disorders which contain the polypeptide.
The polypeptide can be used in the treatment of blood disorders such
as leukemia. The present sequence encodes the protein sequence from
pCHOM1 MABL1-scrV, which is used in an example from the present
invention.

Sequence 819 BP; 208 A; 195 C; 223 G; 193 T; 0 other;

Query Match 62.8%; Score 521.4; DB 21; Length 819;
Best Local Similarity 81.8%; Pred. No. 6,1e-138;
Matches 632; Conservative 0; Mismatches 126; Indels 15; Gaps 2;

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Db      |||||
26 tcttgtagaacaacagcagagtgtagaccacaggttcacgcagcagcagcttgagctg 85
QY      95 agctgtagagggcctgggcttcagtgagctgtccctgcgaagcttcgggctacacatta 154
Db      |||||

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Db      86 acctggtaaagccttgggcttcagtgaaagtcttcgaaaggctcttggatcaccttcg 145
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Db      |||||
146 ttaacctgtatgacacttggtgaagcagacaccccgagggagccttgagtgattgagat 205
QY      215 ctattgacctgaacttggtgtagctgctacaatcagaagttcaaggacagggccatag 274
Db      |||||
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QY      275 tgaactgaagaacactcctcagacagctacatgagctgcgcagcctgcagctgaactgag 334
Db      |||||
266 tgaactgaagaacactcctcagacagctacatgagctgcgcagcctgcagcctgcagtg 325
QY      335 actctgcgctctactctatacaagaatgg-----ttgaagacttggggccaaag 382
Db      |||||
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QY      383 ggaactggtcactgctctgca---gaggtgaatccctcagagatctgcccgaatcca 439
Db      |||||
386 gaaccaactcctcagagctcctcagtggtggtggtcggtggtggtcggtggtggtggtg 445
QY      440 aaccocggagatgtgtgtagaaccccaaccacactcctcctgctgtcagcttggagatc 499
Db      |||||
446 gcgagatcgatgtgtgtagaaccccaaccacactcctcctgctgtcagcttggagatc 505
QY      500 aagctccatctcttcagatcagtcagacagcctttaaagatagatgaatgaatccatct 559
Db      |||||
506 aagctccatctcttcagatcagtcagacagcctttaaagatagatgaatgaatccatct 565
QY      560 tacattgtaacctgcagaaagccagagccaaagctcctcctgatacacaagaatttcca 619
Db      |||||
566 tacaatgtaacctgcagaaagccagagccaaagctcctcctgatacacaagaatttcca 625
QY      620 accgatttcttggtggtcccaagaaggttcaagtgcagtgatcaagagacagattccaac 679
Db      |||||
626 accgatttcttggtggtcccaagaaggttcaagtgcagtgatcaagagacagattccaac 685
QY      680 tcaagatcaagcagagtgagagctgagatctggagattattctgctcctcaagaatcac 739
Db      |||||
686 tcaagatcaagcagagtgagagctgagatctggagattattctgctcctcaagaatcac 745
QY      740 atgttcgtaacgttcgagagggggagccaagcttggaaataaagaagaanaa 792
Db      |||||
746 atgttcgtaacgttcgagagggggagccaagcttggaaataaagaagaanaa 798

```

RESULT 5

AAA92444 standard; DNA: 819 BP.

AAA92444;

15-JAN-2001 (first entry)

Plasmid pCHOM2 MABL2-scrV nucleotide sequence SEQ ID NO:25.

Monoclonal antibody; MABL; IAP; integrin associated protein;
single stranded Fv; apoptosis; blood disease; leukemia;
cytostatic; ds.

Mus sp.

WO200053634-A1.

14-SEP-2000.

10-MAR-2000; 2000WO-JP01458.

10-MAR-1999; 99JP-0063557.

(CHUS) CHUGAI SEIYAKU KK.


```

Db 106 cctggcgctcagtgaaagatatacctcgaaggcttcgtgtactactcattcactgaactaac 165
QY 166 ataacggtgtgaagcgacacacctgtcagtcgtgaatgtgaatgtgaatgtgaatgtgaat 225
XX 166 atgaacgtgtgaagcgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 225
Db 226 gaaactgtgtgtactgtcctcaatcagaagttcaagagcaaggcagcagcagcagcagcagc 285
QY 226 tactatgtgtgtactgtcctcaatcagaagttcaagagcaaggcagcagcagcagcagcagc 285
Db 286 aatcccccacacagcctcactcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 345
QY 286 aatcccccacacagcctcactcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 345
Db 346 tattaactatacaagatgtgttgagggagcagcagcagcagcagcagcagcagcagcagcagcagc 405
QY 346 tattaactatacaagatgtgttgagggagcagcagcagcagcagcagcagcagcagcagcagcagc 405
Db 406 gaggtgaatcctcagatctgtgtcgaatcgaaccccg-----ggatgtgtg 456
QY 406 gaggtgaatcctcagatctgtgtcgaatcgaaccccg-----ggatgtgtg 456
Db 457 atgaccccaaacccactctcctgtcgtcagctgtgagatcgaagcctcctcctgtc 516
QY 457 atgaccccaaacccactctcctgtcgtcagctgtgagatcgaagcctcctcctgtc 516
Db 466 ctaactcagctcactcctcctcgtcgtcagctgtgagatcgaagcctcctcctgtc 525
QY 466 ctaactcagctcactcctcctcgtcgtcagctgtgagatcgaagcctcctcctgtc 525
Db 517 agatctgtcagagccttcttaacagtaagagatacactatttaattgtgactgtcag 576
QY 517 agatctgtcagagccttcttaacagtaagagatacactatttaattgtgactgtcag 576
Db 526 agactatgtcagagccttcttaacagtaagagatacactatttaattgtgactgtcag 585
QY 526 agactatgtcagagccttcttaacagtaagagatacactatttaattgtgactgtcag 585
Db 577 aagcagcagcagctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 636
QY 577 aagcagcagcagctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 636
Db 586 aagcagcagcagctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 645
QY 586 aagcagcagcagctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 645
Db 637 ccaagcagcagctcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 696
QY 637 ccaagcagcagctcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 696
Db 646 ccagcagcagctcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 705
QY 646 ccagcagcagctcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 705
Db 697 gagcctgagagctcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 756
QY 697 gagcctgagagctcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 756
Db 706 gagcctgagagctcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 765
QY 706 gagcctgagagctcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 765
Db 757 ggaagggggggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 804
QY 757 ggaagggggggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 804
Db 766 ggttgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 825
QY 766 ggttgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 825
Db 805 gagatctgaat 816
QY 805 gagatctgaat 816
Db 826 gagatctgaat 837
QY 826 gagatctgaat 837

```

```

PF 09-JUL-1999; 99WO-EP04838.
XX
PR 10-JUL-1998; 98EP-0112867.
XX
PA (CONN-) CONNEX GMBH.
XX
PI Reiter C;
XX
DR WPI; 2000-160926/14.
XX
DR P-PSDB; AAY78328.
XX
PT New oligonucleotide, polypeptide, antibody useful for treating
PT autoimmune disease, immune deficiencies, T-cell malignancies and
PT infectious diseases
XX
PS Example 9; Page 74; 79pp; English.
XX
CC The present invention describes a nucleic acid molecule (I) encoding at
CC least one complementary determining region (CDR) of a variable region of
CC an antibody which specifically interacts with the extracellular domain of
CC the human zeta-chain. The antibody whose CDR of a variable region is
CC encoded by (I), is obtained by immunising a rat with Jurkat cells and
CC subsequently with a conjugate comprising a carrier molecule and a
CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
CC anti-zeta-chain antibody is useful for the treatment and prevention of
CC autoimmune diseases, immune deficiencies, T-cell malignancies,
CC infectious diseases and the suppression of immune response preferably in
CC order to avoid graft rejection after organ transplantation, malignancies,
CC or viral infections. The antibody and fragments of it, can be useful for
CC the enhancement or suppression of NK-cell dependent immunity or for the
CC treatment of NK-cell derived malignancies. It can also be useful for the
CC determination of zeta-chain or eta-chain expression on NK-cells,
CC T-lymphocytes or their precursors. The present sequence encodes a
CC bispecific anti-zeta-chain/anti-EpCAM antibody, from an example from
CC the present invention.
XX
SQ Sequence 1637 BP; 398 A; 404 C; 436 G; 399 T; 0 other;

```

Query Match 60.4%; Score 501.2; DB 21; Length 1637;
 Best Local Similarity 81.4%; Pred. No. 4,1e-133;
 Matches 619; Conservative 0; Mismatches 108; Indels 33; Gaps 2;

```

QY 57 tgccttgcggcggttaactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 116
Db 810 tgccttgcggcggttaactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 869
QY 117 agtgcagcttgcctgcagagccttcgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 176
Db 870 agtgcagcttgcctgcagagccttcgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 929
QY 177 gagcagacacctgtgacatgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 236
Db 930 gagcagacacctgtgacatgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 989
QY 237 tactgcataaatacgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 296
Db 990 tactgcataaatacgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1049
QY 297 cacagcctataatgagctccgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 356
Db 1050 cacagcctataatgagctccgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1109
QY 357 aagatgg-----ttggagcctggggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 386
Db 1110 aagcagggagtcctacagatacctaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1169
QY 387 tctgtacactgtctgtca---gaggttaaatcctcgaagcagcagcagcagcagcagcagcagcagcagc 443
Db 1170 cagcgtacagctcctcccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1229
QY 444 cgggagatgtgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 503

```


XX Herr JC, Norton EJ, Diekman AB;
PI
XX WPI; 2001-182730/18.
DR

PT New recombinant antibody derivative of monoclonal antibody 519, useful
PT as a reagent for purifying or detecting human spermatozoa, as an active
PT ingredient of a spermistatic agent, or as a component of a spermicidal
PT contraceptive -

PS Claim 33; Page 40; 48pp; English..

CC The present invention relates to a recombinant antibody capable of
CC specifically binding to sperm agglutination antigen-1 (SAC-1).
CC The recombinant antibody has two peptide fragments of the S19
CC antibody and the fragments are joined together by a linker.
CC The recombinant monoclonal antibodies are useful in a passive
CC immuno conjugation for contraception as they inhibit the ability of
CC sperm to fertilize an egg. The antibodies may be used e.g. as an
CC active ingredient of a spermstatic agent, or as a component of a
CC spermicidal contraceptive.

Sequence 792 BP; 154 A; 231 C; 224 G; 183 T; 0 other;

Query Match	53.5%;	Score 444;	DB 22;	Length 792;
Best local Similarity	77.3%;	Pred. No. 5e-116;		
Matches 572; Conservative	0;	Mismatches 150;	Indels 18;	Gaps 2

Oy	62	ttgagcgcggttcaactgcagcagcagctctgggctctgaagctctgtgaagcctctgggcttcaatga	121
Db	2	ttggccaagtggaactgcagcaactctggcttgcttgcaaccgggtgcccccttgcccttcaatga	61
Oy	122	cgctctcttcaagagcttcctggctctacaacatttactgacatgaatcaacacgggttgagcg	181
Db	62	aggtgtcctctggcgcttccttgctctacaattccacaactactagtatgacatcggtggcgcc	121
Oy	182	agaaactctgacatggcctcggaatggaattgagctatttgatctctgaactctgtgtactg	241
Db	122	agcgccctggcccaagggccccctggagtgagatctggcgatattatctctgttaagtgatctcta	181
Oy	242	ccctcaatcagaagtttcaagaggaagcgcccaatgagatgagatgagaagaattctccagacag	301
Db	182	actcaggttgagatctcaagaacaagcgcaacactgagatgaagcaatctccagacag	241
Oy	302	ccctcaatggagctctcccgcaacccctgaaatctgaaagctctggcgtcttacttacaatcaaat	361
Db	242	tttctcatccaaactcagcagccctgaaatctgaaagctccggctcgtctattctctgtcaagag	301
Oy	362	gg-----tttgaagactggggccaagggactctgctacgtctc--tg	403
Db	302	ggagctatggttccctctgtttcttactgggccaaggaacccaaggtcttaccacgtctcaatg	361
Oy	404	cagaaggtaatcctcagatctgctcgcagatcccaaccggggagttgttgatgaacc	463
Db	362	ggcgcgcgagcagcaggtgtgtgtgttcttgggcgggcgagcgagacatcagatccatc	421
Oy	464	caaacccactctccctgctgtcagttcttgagatcaagaacctccatctcttgcaactcta	523
Db	422	agttccatctctccgcgtctgcaatctcttgcgatccagatccatctcttccgctcta	481
Oy	524	gtcagcaacctttaaacaataatggaatcaacctattacaattgtaacctgcagaaagcag	583
Db	482	gtcagagttctgtaacacagtaatctggcacactatctgactgttctctgcagaagccag	541
Oy	584	gccagcttccaaagctccctgcatactacaagaatttccaaccgatcttctgggggtcccaagca	644
Db	542	ggcagcttcccaagggccctgcatactacogcggttccaacggcttctctgggggtcccaagcc	601
Oy	644	gtttcagttggcagtgtatcagaagaaatttcaacatccaaagatccagacagtgtagcgctg	703
Db	602	gtttcattatggcaatgctcagaagaaatttcaacatccaaagatccaaacacgtgtgagcgctg	661

Accession	Sequence	Position
QY	704 agagatctgggaatttatcttcgcctcaagaatcaatgcttcgcgaaggg	763
Dd	662 agagatctgggcgtttatcttcgcctcaagaatcaatgcttcgaaggg	721
QY	764 ggaaccaagctggaataa	783
Dd	722 ggaaccaagctggaatca	741

RESULT 14

ID AAF60026 standard; DNA; 786 BP.

AC AAF60026;

DT 26-APR-2001 (first entry)

DE DNA encoding single chain Fv fragment #4

KW Antibody; sperm; S19; contraception; ds.

OS Synthetic

PN WO200107083-A1

PD 01-FEB-2001

PF 21-JUL-2000; 2000WO-US19843.

PR 23-JUL-1999; 99US-0145512.

PA (UYVI-) UNIV VIRGINIA PATENT FOUNDD

PI Herr JC, Norton EJ, Diekman AB.

DR WPI; 2001-182730/18.

PT New recombinant antibody derivative of monoclonal antibody S19, useful
PT as a reagent for purifying or detecting human spermatozoa, as an activator
PT ingredient of a spermstatic agent, or as a component of a spermicidal
PT contraceptive -

PS Claim 36; page 45-46; 48pp; English.

The present invention relates to a recombinant antibody capable of specifically binding to sperm agglutination antigen-1 (SAGA-1). The recombinant antibody has two peptide fragments of the S19 antibody and the fragments are joined together by a linker. The recombinant monoclonal antibodies are useful in a passive immunization composition for contraception as they inhibit the ability of sperm to fertilize an egg. The antibodies may be used e.g. as an active ingredient of a spermstatic agent, or as a component of a spermicidal contraceptive.

Sequence 786 BP; 153 A; 229 C; 222 G; 182 T; 0 other;

Query Match	53.4%	Score 443.4;	DB 22;	Length 786;
Best Local Similarity	77.6%;	Pred. No. 7.3e-116;		
Matches 569;	Conservative 0;	Mismatches 146;	Indels 18;	Gaps 2;

QY	69	ggtctcaacgcgaacagctcctgggagctgcagcctgcgaagcctcgttcacgtacgcctc	123
Db	3	ggctaaacctgcacaaacctggctcgaacacggctgcgcccgagctcccaagatgaatgctc	62
QY	129	ctgcaagagcttcggcgtaacacattactgcatatgaatacacttcggctgcgaagacac	186
Db	63	ctgcgcgccttcgcgtataaattacacacctacttgatgcatttcggctgcgcacgcgc	122
QY	189	tgttcacgcgcttcgaatgcattgcagcctatgcctccgaacacgcgcgcgcctctaca	244
Db	123	tgcgcgaagcgccctgaatgcattgcgcataattacacctgcgcgcgcgcgcgcattcaactaga	187

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CM nucleic - nucleic search, using sw model

Run on: January 17, 2002, 23:53:12 ; Search time 44.35 Seconds
(without alignments)
4238.483 Million cell updates/sec

Title: US-09-358-321C-31

Perfect score: 830
Sequence: 1 tctagaatgtaagcgctat.....ctgaatgaagcgagcgcg 830

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	380.4	45.8	772	1 US-08-331-398A-33	Sequence 33, Appl
2	380.4	45.8	772	2 US-08-331-397B-33	Sequence 33, Appl
3	380.4	45.8	772	2 US-08-759-804A-33	Sequence 33, Appl
4	380.4	45.8	772	4 US-09-227-693-33	Sequence 31, Appl
5	349	42.0	741	4 US-09-227-693-31	Sequence 31, Appl
6	348.2	42.0	738	1 US-08-331-398A-31	Sequence 31, Appl
7	348.2	42.0	738	2 US-08-331-397B-31	Sequence 31, Appl
8	348.2	42.0	738	2 US-08-759-804A-31	Sequence 31, Appl
9	347.4	41.9	2010	3 US-09-070-637-19	Sequence 19, Appl
10	338.8	40.8	814	2 US-08-752-844-65	Sequence 65, Appl
11	337.2	40.6	831	2 US-08-403-853-17	Sequence 17, Appl
12	332.6	40.1	1095	3 US-08-875-811-52	Sequence 52, Appl
13	332.6	40.1	1098	3 US-08-875-811-54	Sequence 54, Appl
14	327.6	39.5	965	1 US-08-388-672A-22	Sequence 22, Appl
15	327.6	39.5	965	3 US-09-080-554-22	Sequence 22, Appl
16	326.4	39.3	891	2 US-08-894-922A-9	Sequence 9, Appl
17	321.8	38.8	907	3 US-09-184-658-9	Sequence 9, Appl
18	321	38.7	797	2 US-08-894-922A-13	Sequence 13, Appl
19	320.4	38.6	384	1 US-08-482-882-44	Sequence 44, Appl
20	320.4	38.6	384	1 US-08-483-389-44	Sequence 44, Appl
21	320.4	38.6	384	2 US-08-487-113D-44	Sequence 44, Appl
22	320.4	38.6	384	2 US-08-473-503-44	Sequence 44, Appl
23	320.4	38.6	384	2 US-08-483-932-44	Sequence 44, Appl
24	320.4	38.6	384	2 US-08-720-420A-44	Sequence 44, Appl
25	320.4	38.6	384	3 US-08-714-017-44	Sequence 44, Appl
26	320.4	38.6	384	3 US-08-475-680-44	Sequence 44, Appl
27	316	38.1	537	5 PCT-US91-02942-2	Sequence 2, Appl

28	316	38.1	537	5 PCT-US91-02946-2	Sequence 2, Appl
29	313.6	37.8	856	4 US-09-318-661-3	Sequence 3, Appl
30	313.6	37.8	856	4 US-09-318-661-6	Sequence 6, Appl
31	313.4	37.8	2165	4 US-08-263-911-8	Sequence 8, Appl
32	312	37.6	1797	1 US-08-463-163-2	Sequence 2, Appl
33	311.6	37.5	720	1 US-08-800-198-7	Sequence 7, Appl
34	311.6	37.5	720	3 US-09-296-595-7	Sequence 7, Appl
35	311.2	37.5	2165	2 US-08-263-911-6	Sequence 6, Appl
36	310.2	37.4	719	3 US-08-279-772A-7	Sequence 7, Appl
37	310.2	37.4	720	3 US-08-902-486-10	Sequence 10, Appl
38	308	37.1	424	3 US-08-589-939-8	Sequence 8, Appl
39	307	37.0	1460	2 US-08-392-338A-18	Sequence 18, Appl
40	307	37.0	1460	3 US-09-166-750-18	Sequence 18, Appl
41	307	37.0	1460	3 US-09-166-093-18	Sequence 18, Appl
42	307	37.0	1460	3 US-09-172-019-18	Sequence 18, Appl
43	307	37.0	1460	3 US-09-166-094-18	Sequence 18, Appl
44	306.4	36.9	394	1 US-07-977-696C-26	Sequence 26, Appl
45	306.4	36.9	394	1 US-08-129-930B-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-08-331-398A-33
Sequence 33, Application US/08331398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:

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NAME/KEY: 1.772
LOCATION: 1.772
OTHER INFORMATION: /note="Single-chain antibody fusion
OTHER INFORMATION: protein of B3 monoclonal antibody
OTHER INFORMATION: Variable Heavy chain (V-H) and
OTHER INFORMATION: Variable Light chain (V-L) Fv region
OTHER INFORMATION: joined by a (Gly-4Ser)-3 peptide linker"
FEATURE:
NAME/KEY: CDS
LOCATION: 27..770
US-08-331-397B-33

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Query Match 45.8%; Score 380.4; DB 1; Length 772;

Best Local Similarity 72.0%; Pred. No. 4.4e-106;

Matches 533; Conservative 0; Mismatches 186; Indels 21; Gaps 2;

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QY 66 ggcgggtcaactgcaagcagctgaggctgagctgtagagcctggggttcagtagcgt 125
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 29 GGATGTGAAGCTGGTGGAGTCTGGGGAGGCTTAGTGCAGCCTGGAGGGTCCCTGAAC 88
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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DB 149 TCCAGAGAGAGAGGCTGGAGTGGGTCCGATACATATATATATATATATATATATATAT 208
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QY 246 caatcagaatcaaggacagccatagtagtagtagtagtagtagtagtagtagtagtagtag 305
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DB 209 TTCAGACACTGTAAAGGCGGTTTCCATCTCCAGAGCAATGCGAGAGAACCCCTCTA 268
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QY 361 -----tggtttagagactggggtgagagagagagagagagagagagagagagagagagag 405
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DB 329 GGCCCTGGGAGCCTGTGTTCTTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 388
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QY 406 -gaaggtaaatcctcagagatctggtccgaatccaaacccgggagatgttgtagatccccc 464
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DB 389 CGGAGGGGAGTCCGGGTGCGGCGGATCTGAGAGTGGCGGAGACGATGTCATATATATAT 448
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QY 465 aaaccacactccctcgctcgtcagatcttgtagatcaagccatccatctcttgagatcag 524
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DB 449 GTCTCCATGAGTGTACCTCTCTGAGTCTGAGATCAAGCCTCCATCTCTTGCAGATCTAG 508
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DB 509 TCACATATGTACATAGTATGTAACACACCTTTTGAATGTATCTGACAGAAACCAAG 568
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DB 569 CCACTCTCCAAAGCTCTGTATCTACAAAGTTTCCAAACGATTTCTGGGGTCCAGAGAG 628
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QY 645 gticagtgagcagtgagtagcagagagagagagagagagagagagagagagagagagag 704
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DB 629 GTTAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 688
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QY 705 gtagctggaggttattctctcgtcctcaagtagacacatgttcgtagcaggttcggagagag 764
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QY 765 gaccagaactggaataaag 784
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DB 749 GACCAAGCTGGAATTTAAG 768
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```

RESULT 2
US-08-331-397B-33
; Sequence 33, Application US/08331397B

```

Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: 1.772
LOCATION: 1.772
OTHER INFORMATION: /note="Single-chain antibody fusion
OTHER INFORMATION: protein of B3 monoclonal antibody
OTHER INFORMATION: Variable Heavy chain (V-H) and
OTHER INFORMATION: Variable Light chain (V-L) Fv region
OTHER INFORMATION: joined by a (Gly-4Ser)-3 peptide linker"
FEATURE:
NAME/KEY: CDS
LOCATION: 27..770
US-08-331-397B-33
Query Match 45.8%; Score 380.4; DB 2; Length 772;
Best Local Similarity 72.0%; Pred. No. 4.4e-106;
Matches 533; Conservative 0; Mismatches 186; Indels 21; Gaps 2;
QY 66 ggcgggtcaactgcaagcagctgaggctgagctgtagagcctggggttcagtagcgt 125
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DB 89 CTCCTGTGCAACCTCTGGATCTCCTTCAGTCACTATTCATGATGTTGGTTCCGACAG 148
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QY 186 acctgtgcatggtcgaatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagat 245
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DB 149 TCCAGAGAGAGAGGCTGGAGTGGGTCCGATACATATATATATATATATATATATATATAT 208
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Db 509 TCACATCATTTGTACATAGTATGAGAAACACCTATTAGATGTAAGTACCTCCAGAACCGAG 568
QY 585 ccagctcccaaaagctcctgatactctacaaagtttccaaacgatttctg999gtcccaagacg 644
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Db 569 CCACTCTCCAAAGCTCCTGATCTACAAAGTTCCAAACCATTTCTGGGGGTCCAGAGACG 628
QY 645 gttaagtggaagtgatcagagaaagatttcacactcaagatcagagagtggaagctga 704
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Db 629 GTTAGTGGCAGTGGATCAGGACAGATTTCACACTCAAGATCAGACAGAGTGGAGGCTGA 688
QY 705 ggaactggaggttattctcgtctcacaagttacacatgttcggtacaggttcggaagggg 764
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Db 689 GGATCTGGAGATTATTACTGCTTCAAGGTTCCACATGTTCCATTCACGTTGCGGTCCGG 748
QY 765 gaccaagctggaataaaag 784
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Db 749 GACAAAGCTGGAATTAAG 768

RESULT 4

US-09-227-693-33
; Sequence 33, Application US/09227693
; Patent No. 6287562

GENERAL INFORMATION:

APPLICANT: PASTAN, Ira
APPLICANT: BENHAR, Itai
APPLICANT: PADLAN, Eduardo A.
APPLICANT: JUNG, Sun-Hee
APPLICANT: LEE, Byungkook
TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,396
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-126-1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 27..767

US-09-227-693-33

Query Match 45.8%; Score 380.4; DB 4; Length 772;
Best Local Similarity 72.0%; Pred. No. 4.4e-106;
Matches 533; Conservative 0; Mismatches 186; Indels 21; Gaps 2;

QY 66 ggcgtgttaactcgaacagctcgtgggtcgtgagctgtgagagccttggtcgttaagcgt 125
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Db 29 GGATGTGAAGCTGTGAGCTCTGGGGAGGCTTAAGTCAGCGCTGAGGGGCTCCGAAACT 88
QY 126 gtctcgaaggtctcgtgtacacattactactaagaaatcacactgtgtgaagcaagc 185
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Db 89 CTCCTGTGCAACCTCGAGATTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 148
QY 186 acctgtgcatggtcgtgaatgagctgtgagagctgtgacctgaaactgtgtgactgcta 245
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QY 246 caatcagaagttcaaggacagccatagtgagctgtgagaaatcctccagacagccta 305
Db 209 TTCAGACACTGTAAAGGCCGGTTCACCATTCACAGACAGCAATGCCAGAACCCCTCTA 268
QY 306 catggaagctcgaagcctgacatcgtgaagactctgcgtctatactatacaaaagc----- 360
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Db 269 CCTGCAATGAGCCGCTGAGCTGAGAGACAGCCATATATCTCTGTGCAAGAGGACT 328
QY 361 -----tggttgaagagctggggccaaagagactcgtgactgtctcgtga-- 405
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QY 406 -gaaggtaaatcctcagagatcgtcccgaaatccaaacccgggagatgtgtgataccccc 464
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Db 389 CGAGAGCGGATCCGGTGGTGGCGGATCGAAGTGGCGGAGAGCATGTGCTATGACCA 448
QY 465 aaaccacatcctcctgctgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 524
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Db 449 GTCTCATTAAGTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 508
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Db 509 TCACATCATTTGTACATAGTATGAGAAACACCTATTAGATGTAAGTACCTCCAGAACCGAG 568
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Db 569 CCACTCTCCAAAGCTCCTGATCTACAAAGTTCCAAACCATTTCTGGGGGTCCAGAGACG 628
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Db 629 GTTAGTGGCAGTGGATCAGGACAGATTTCACACTCAAGATCAGACAGAGTGGAGGCTGA 688
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Db 689 GGATCTGGAGATTATTACTGCTTCAAGGTTCCACATGTTCCATTCACGTTGCGGTCCGG 748
QY 765 gaccaagctggaataaaag 784
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Db 749 GACAAAGCTGGAATTAAG 768

RESULT 5
US-09-227-693-31
; Sequence 31, Application US/09227693
; Patent No. 6287562
GENERAL INFORMATION:
APPLICANT: PASTAN, Ira
APPLICANT: BENHAR, Itai
APPLICANT: PADLAN, Eduardo A.
APPLICANT: JUNG, Sun-Hee
APPLICANT: LEE, Byungkook
TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourile and Crew
 STREET: Stewart Street Tower, One Market Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94105-1493
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/227,693
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/331,396
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/767,331
 FILING DATE: 30-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/596,289
 FILING DATE: 12-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen Lauver
 REGISTRATION NUMBER: 32,762
 REFERENCE/DOCKET NUMBER: 15280-126-1-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 741 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1..741
 OTHER INFORMATION: /note= "Sequence encoding humanized
 Patent No. 6287562
 OTHER INFORMATION: B3(FV)"
 US-09-227-693-31

Query Match 42.08; Score 349; DB 4; Length 741;
 Best Local Similarity 69.48; Pred. No. 1.5e-96;
 Matches 513; Conservative 0; Mismatches 205; Indels 21; Gaps 2;

Db 303 GGCTGGGAGACCTGTGTTCTTACTGCGGCCAAGGAGACTGTGTCATGTTCTCTCAAG 362
 Qy 406 -gaaggtaaatcctcaagatctgtctcgatccaaacccggagatgttgatgacccc 464
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 Db 423 GTCTCCATTGAGTTTACTCTACCCCGGAGGAGCGGCTCCATCTCTGGAGATCTAG 482
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 Db 543 CCAAGTCTCCACAGCTGCTGATCTAAGAGTTTCCAACCCATTTCTGGGGTCCACAGAG 602
 Qy 645 gttaagtggaagtgatcaagagacagattcacactcaagatcaagagtgagagctga 704
 Db 603 GTTCAGTGGCAGTGTGATCAGGAGACAGATTTCACACTCAAGATCAGCAGATGAGCTGA 662
 Qy 705 ggaactggagattatctctgctctcaagatacacatgttccgtacacglttcgaggg 764
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 Db 723 TACCAAGTCCGAATTAA 741

RESULT 6
 US-08-331-398A-31
 Sequence 31; Application US/08331398A
 Patent No. 5608039
 GENERAL INFORMATION:
 APPLICANT: Pastan, Ira
 APPLICANT: Willingham, Mark
 APPLICANT: Fitzgerald, David
 APPLICANT: Brinkmann, Ulrich
 APPLICANT: Pal, Lee
 TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
 NUMBER OF SEQUENCES: 68
 NUMBER OF INVENTIONS: and Their Uses (as amended)
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew
 STREET: One Market Plaza, Stewart Street Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105-1492
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/331,398A
 FILING DATE: 28-OCT-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/767,331
 FILING DATE: 30-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/596,289
 FILING DATE: 12-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 015280-1261100S
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043

Db 724 AAGTCGAATTAA 738
RESULT 7
US-08-331-397B-31

QY 190 gtagcagccctggaatagatgagccttgcacccaacgtgtagtgcctcaat 249
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QY 250 cagaagtcaagagacagagccctatgagcttgaagaaatcccccgaagagctatag 309
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DB 118 AGCCTGTCATACATGACATGCTGTCAGGCTTCTCATTAACCACTATGAGTAAAGCTG 177
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DB 475 ATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 534
QY 517 AGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 576
DB 535 AGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 594
QY 577 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 636
DB 595 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 654
QY 637 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 696
DB 655 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 714
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DB 715 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 774
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DB 775 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 804

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RESULT 11
US-08-403-853-17
; Sequence 17, Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORT, Alex A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALBY, Robyn L.
; APPLICANT: POWER, Barbara E.
; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,853
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU93/00491
FILING DATE: 24-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 4973
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/189/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 831 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: mat-peptide
LOCATION: 1..819
FEATURE:
NAME/KEY: CDS
LOCATION: 1..819
US-08-403-853-17
Query Match 40.6%; Score 337.2; DB 2; Length 831;
Best Local Similarity 67.7%; Pred. No. 6e-93;
Matches 524; Conservative 0; Mismatches 208; Indels 42; Gaps 2;

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? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/875,811
? FILING DATE: 19-FEB-1998
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: WO PCT/US97/02588
? FILING DATE: 19-FEB-1997
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 60/011,800
? FILING DATE: 21-FEB-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Faris, Susan K.
? REGISTRATION NUMBER: 41,739
? REFERENCE//DOCKET NUMBER: 015280-244100US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 54:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1098 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1098
? OTHER INFORMATION: /note="MOC31FBmetseronc"
US-08-875-811-54

Query Match 40.1%; Score 332.6; DB 3; Length 1098;
Best Local Similarity 68.2%; Pred. No. 1.7e-91;
Matches 496; Conservative 0; Mismatches 219; Indels 12; Gaps 2;

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QY 537 acacagtaatgatgataccatttaacattgtgtactgcagaagccagccagctctccaa 596
DB 486 ACATAGTAATGAGCATCATCTATTGTATGTGATCTGACAGAACCCAGCCAGTCTCCCA 545
QY 597 gccctgatactacaagttccaacccgatttctcgtgggtcccaagcaggttcagtgag 656
DB 546 GCTCCGATTTATTCAGATGCTCCAACTTGCCTCAGAGATCCGACAGAGTTCCAGTAGCAG 605
QY 657 tggatcaggagagagatttcaacactcaagatcaagagtgagagtgctgagatctggaggt 716
DB 606 TGGGTCAAGACATGATTTCACACTGAGATCAAGACAGAGAGGCTGAGATGTGGTGT 665
QY 717 ttattctgtctcaaaagtacacatgttccgtacacgttcggagggggagccagctgga 776
DB 666 TTAATTAAGTGTCTCAAAATCTAGAAATTCCTGACAGTTCGGTGGAGGACCAAGCTGGA 725
QY 777 aataaaa 783
DB 726 AATCAAA 732

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RESULT 14
US-08-388-672A-22
Sequence 22, Application US/08388672A
Patent No. 5795961
GENERAL INFORMATION:
APPLICANT: Wallace, T. Paul
APPLICANT: Harris, William J.
APPLICANT: Carr, Frank J.
APPLICANT: Old, Lloyd J.
APPLICANT: Welt, Sydney
APPLICANT: Kitamura, Kunio
TITLE OF INVENTION: Recombinant Human Anti-Lewis B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Felle and Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,672A
FILING DATE: 14-FEB-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5795961man D.
REGISTRATION NUMBER: 30,946
REFERENCE//DOCKET NUMBER: LUD 5409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 965 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-388-672A-22

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Query Match 39.5%; Score 327.6; DB 1; Length 965;
Best Local Similarity 71.6%; Pred. No. 5.3e-90;
Matches 563; Conservative 11; Mismatches 127; Indels 85; Gaps 8;

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Db 468 CACGTAATGASCSRSSTHNGGAAACACCTATTATATGATGCTGAGAAACAGG 527
Qy 585 ccagtcctccaaag-----ctcctgattacaagtttcacacgatttctg9g 634
Db 528 CCAGTCTCCAAAGNTTYWYKSKTCTGATCTACAGGGTTTCCAAACGATTTCTGGGG 587
Qy 635 tcccaagacaggt-----cagtgagagtgatcagggacagatttcacactcaa 683
Db 588 TCCAGACAGGTTTYSNBSGVDRCAAGTGACAGTGCAGGACAGATTTCACACTCAA 647
Qy 684 gatcagcagagtg-----aggctgagatctggagtttattctgcttc 730
Db 648 GATCAGCAGAGTGGSGSGTDTKSRVAGGCTGAGGATATGGGAGTTTATCTGCTTC 707
Qy 731 aaatcacatgttcgctac-----acgttcgagggggaccagctggaaa 778
Db 708 AAGGTACACATGCTCTADMGVYCCGTHACGACGTTCCGTGAGGACCAAGCTGGAAA 767
Qy 779 taaaag 784
Db 768 TCAAAR 773
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Search completed: January 18, 2002, 00:41:15
Job time: 2883 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 17, 2002, 23:48:02 ; Search time 1210.51 Seconds

(without alignments)
7367.966 Million cell updates/sec

Title: US-09-358-321c-31

Perfect score: 830
Sequence: 1 tctagaatgtaagcgcctat.....ctgaattagtaagcgcgcg 830

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372869281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthm:*
3: em_estlin:*
4: em_estom:*
5: em_estopl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hnc:*
10: gb_estl:*
11: gb_est2:*
12: gb_hnc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	316	38.1	678	11	BG962941 602827925
2	316	38.1	925	11	BG963141 602828165
3	314.4	37.9	997	11	B1107100 602894523
4	312.2	37.6	962	11	BF578262 602093093
5	309.2	37.3	793	10	BE307894 601096548
6	308	37.1	693	11	BG964281 602829076
7	302.2	36.4	716	11	BG964192 602828968
8	300.2	36.2	743	11	BG968770 602836677
9	296.6	35.7	965	11	BF577927 602091947
10	280.8	33.8	509	13	AZ791472 2M0041H3
11	279.6	33.7	898	11	BF135785 601782072
12	278.2	33.5	755	11	B1109046 602896879

13	277.8	33.5	884	11	BG963735
14	276.6	33.3	772	10	BE285427
15	276.4	33.3	707	11	B1250555
16	247	29.9	766	11	BG969524
17	240.6	29.0	512	11	BF023434
18	240	28.9	723	11	BG969577
19	240	28.9	952	11	BG758592
20	236.4	28.5	1576	12	AK007918
21	233.6	28.1	471	10	AA405772
22	232	28.0	614	10	AA405187
23	228.6	27.5	454	10	AA406683
24	228	27.5	909	11	B1105366
25	227.2	27.4	886	11	BG963760
26	227	27.3	967	11	BG964352
27	226	27.2	491	11	BF174573
28	225.4	27.2	751	11	BG542438
29	224.4	27.0	598	11	B1104341
30	224.4	27.0	829	11	BF144014
31	223.8	27.0	363	10	AA464313
32	223.8	27.0	488	10	AA405725
33	223.6	26.9	739	10	BE284158
34	223.4	26.9	488	11	H25625
35	223.2	26.9	773	11	BG964451
36	222.2	26.8	410	11	BG059215
37	222.2	26.8	880	11	BG555003
38	222.2	26.8	880	11	BG575788
39	221.4	26.7	463	11	BF150860
40	221.2	26.7	743	11	BF168514
41	221.2	26.7	889	11	BF134160
42	220.6	26.6	400	10	AW612881
43	220.6	26.6	425	10	A1734035
44	220.6	26.6	432	11	BF095363
45	220.6	26.6	442	10	AA405415

ALIGNMENTS

RESULT 1
BG962941 678 bp mRNA EST 12-JUN-2001
LOCUS 602827925F1 NC1_CGAP_Co24 Mus musculus cDNA clone IMAGE:4982670 5',
DEFINITION
ACCESSION BG962941 GI:14350578
VERSION BG962941
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE
1 (bases 1 to 678)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-femail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10986 row: a column: 07
High quality sequence stop: 676.
Location/Qualifiers
1. 678
/organism="Mus musculus"
/strain="TVB/N"
/dd_xref="taxon:10090"
/clone="IMAGE:4982670"
/clone_id="NC1_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"

BASE COUNT	156	a	210	c	217	g	210	t
ORIGIN	/note="Organ: mammary; Vector: PCMV-SPORT6; Site1: SalI Site2: NotI; Cloned unidirectionally. Primer: Oligo dr library constructed by life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"							

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/Notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."
BASE COUNT      179 a      184 c      160 g      169 t
ORIGIN

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	Best Local Similarity	94.7%;	Pred. No. 4,9e-78;		
	Matches 320;	Conservative	0;	Mismatches 18;	Indels 0; Gaps
OY	446 gggatgttgtagatgaccccaaccacatctcccgcgtctcagttcttggagaaccaagcct				505
Db	80 GTGATGTGGATACCCAAACTCCACTCCTCGCTTCACTTGAGATGAACAGCT				139
OY	506 ccactctcttgagaatactagtcagagaccttttacaaqtaigaattcacatctaactt				565
Db	140 CCACTCTCTGTAGATTCTAGTCAGACGCTTTTAACAGATAATGGAAACACTTTTACATT				199
OY	566 ggtaacctcgacaagaagccaggccagtctccaagctctctgaactacaagtttccaacgat				625
Db	200 GGTTCTCGCAGAAGCCAGGCCAGTCTCCAAAGCTCTGTACAACAGAGTTTCCAACCAT				259
OY	626 ttctctggagttccccagaagaagttltaagtcagtcagtcagaagaagaatttcaaatccaaga				685
Db	250 TTTCTGGGGTCCAGACAGSTTCAAGTGGCACTGTGATCAAGGACAGATTTCACACTCAAGA				319
OY	686 tcagcaagaatggagaagctgaagatcttggaatttatcttgcctctcaaaagtatacatgtctc				745
Db	320 TCACCAAGATGGAGGCTGAGAGATCTGGGGATTATTTCTGCTCTCAAAGTACACATGTGTC				379
OY	746 -cgatacgtctcgagagggggagccaacatctgaaaataaa				783
Db	380 CGCTCACGTTCCGCTGCTGGAGCCAAAGCTGGAGCTGAAT				417

RESULT	6
LOCUS	BG964281
DEFINITION	BG964281 693 bp mRNA
ACCESSION	602839076F1 NC_01_CGAP_C024 Mus musculus cDNA clone IMAGE:4983618 5'
VERSION	BG964281
KEYWORDS	BG964281.1 GI:14351918
SOURCE	EST.
ORGANISM	house mouse.
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Rodentia; Sclerothachi; Muridae; Murinae; Mus
JOURNAL	1 (pages 1 to 693)
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov Tissue Procurement: jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.jnl.gov plate: LLAM10968 row: h column: 19 High quality sequence stop: 553.

[illegible]

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Location/Qualifiers
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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/cname="IMAGE:4983618"
/clone_1b="NCL_CGAP_CO24"
/lab_most="DH10B (T1 phage-resistant)"
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source
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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_name="IMAGE:4983617"
/clone_lib="NCI-CCAP-Co2a"
/ab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-Sport6; Site:1; NotI;

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Site 2: SalI: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP Library."

BASE COUNT 191 a 188 c 163 g 174 t
ORIGIN

Query Match 36.4%; Score 302.2; DB 11; Length 716;
Best Local Similarity 94.6%; Pred. No. 5e-76;
Matches 313; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 453 tctgatacccccaaccactctccctgcctgcctgagcttgagatcaagcctcatctc 512
DB 97 TGTGTGACCCCAACTCCACTCTCCCTGCTGCACTGTGAGATCAAGCCCTCATCTC 156
QY 513 ttgagatctagatcagagcctttacacagtaatgaaacacactatttcattgttact 572
DB 157 TTGCAGATCTAGTCAAAACCTTGACACATATGGAACACCTATTTCATTGTACT 216
QY 573 gcaagaagccaaagccagctcccaagctcctgactcacaagttcccaacgatttctgg 632
DB 217 GCAGAGGCCAGGCGAGCTCCAAAGCTCTGATCTACAAAGTTCCACCGATTTCCTGG 276
QY 633 ggtccagacaggttcctgagctgagatcagagacagatttacaactcaagatcgag 692
DB 277 GGTCCACACAGGTTCACTGAGTGCATGAGGACAGATTTCACACTCAAGTCCAGAG 336
QY 693 agtgaagctgaagatctggaagttattctctcctcacaagacacatgctccgacac 752
DB 337 AGTGAGGCTGAGGATCTGGGAGTTATTCTGCTCAAAATACACATGTCCTCGTGAC 396
QY 753 gttcgaagggggaaccaaagctggaataaaa 783
DB 397 GTTCGTGAGGACACCAAACTGGAATCAAA 427

RESULT 8
LOCUS BG968770 743 bp mRNA EST 12-JUN-2001
DEFINITION 602836677F1 NCI-CGAP-Co24 Mus musculus cDNA clone IMAGE:490962 5',
ACCESSION BG968770
VERSION BG968770
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM11007 row: j column: 19
High quality sequence stop: 659.
Location/Qualifiers
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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:490962"
/clone_id="NCI-CGAP-Co24"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: colon; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

FEATURES
Source

1..743
Location/Qualifiers
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:490962"
/clone_id="NCI-CGAP-Co24"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: colon; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP Library."

BASE COUNT 199 a 196 c 181 g 167 t
ORIGIN

Query Match 36.2%; Score 300.2; DB 11; Length 743;
Best Local Similarity 94.4%; Pred. No. 1.9e-75;
Matches 322; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 444 cggagatgtgtatgatacccccaaccactccctgcctgcctgagcttgagatcaagc 503
DB 68 CAGGATGTTGTATGATGCCAAACTCCACTCTCCCTGCTGCACTGTGAGATCAAGC 127
QY 504 ctccatctctgagatcagatcagagcctttacacagtaatggaatcaactattaca 563
DB 128 CTCATCTCTGCGAGATCTAGTCAGAGCCCTGTACACACTAATGGAACACCTATTACA 187
QY 564 ttgtacctgcaagaagccagcagctctccaagctccctgactcacaagtttcaaccg 623
DB 188 TTGTACTCTCAGAGCCAGGCGAGCTCCAAAGCTCTGCTACAGATTCCACCG 247
QY 624 attctcggggtcccaagacaggttcagctgagatcagagacagatttcaactcaa 683
DB 248 ATTTCTGGGGTCCACACAGTTCACTGCTGCACTGATGAGGACAGATTTCACACTCA 307
QY 684 gatca-gcaagatgagagctcagagatctgggaagttattctgctcacaagatcacatg 742
DB 308 GATCAGCTAGAGTGGAGGCTGAGGATCTGGGAGTTATTCTGCTCAAAATACACATG 367
QY 743 ttccgtacagcttcgagggggggaacaaagcttggaataaaa 783
DB 368 TTCCGCTCAGCTTGCTGCTGAGACCAAGCTGAGCTGAAA 408

RESULT 9
LOCUS BF577927 965 bp mRNA EST 12-DEC-2000
DEFINITION 602091947F1 NCI-CGAP-Co24 Mus musculus cDNA clone IMAGE:4206515 5',
ACCESSION BF577927
VERSION BF577927
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9767 row: m column: 12
High quality sequence stop: 665.
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/db_xref="taxon:10090"
/clone="IMAGE:4206515"
/clone_id="NCI-CGAP-Co24"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: colon; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life

FEATURES
Source

1..965
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:4206515"
/clone_id="NCI-CGAP-Co24"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: colon; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life

Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://Image.lnl.gov>
 Plate: L1AM1369 row: k column: 04

FEATURES

SOURCE

High quality sequence stop: 707.
 Location/Qualifiers

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 /db_xref="taxon:10090"
 /clone="IMAGE:5149563"
 /clone_id="NCI CGAP Mam5"
 /tissue_type="tumor_gross tissue"
 /dex_stage="7 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

BASE COUNT 198 a 171 c 172 g 166 t
 ORIGIN

Query Match

Best Local Similarity 33.3%; Score 276.4; DB 11; Length 707;
 Matches 326; Conservative 87.2%; Pred. No. 1,3e-68; Mismatches 46; Indels 2; Gaps 2;

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Db 4 GTTGGTGCTGAGATGTTCTGATTCCTGATTCATCAGGATGATGTT-TGATGACCCAACTC 62

QY 470 caactcctcctgctcagctcgttgagataaagctccatctcttcagatctagtcaga 529
    || || || || || || || || || || || || || || || || || || || || ||
Db 63 CACTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 122

QY 530 gcccttaacacagtaatggaatcaactatctgtaactgacagaaagccagccagt 589
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Db 123 ACATGTT-CATAGTAATGGAACACCTATTAGATGATGCTGACAGAGCCAGCCAGT 181

QY 590 ctccaaagctcctgctcctcacaagttccaaacgattctcggggtcccaacaggtca 649
    || || || || || || || || || || || || || || || || || || || || ||
Db 182 CTCCTAAAGCTCCTGATCCACAAAGTTTCCAAATAGATGTTGTGGGGTCCCAAGACGTTCA 241

QY 650 gtggcagtgatcaaggacagatctcacactcaagatcagagagtgaggctgaagatc 709
    || || || || || || || || || || || || || || || || || || || || ||
Db 242 GTGGCAGTGATCAGGAGCAAAATTTCACACCTCAGGGTCCAGAGTGGAGGCTGAGGATC 301

QY 710 tgggaatttattctgctcctcaagataacatgttcgttacagcttcggagaggaggaca 769
    || || || || || || || || || || || || || || || || || || || || ||
Db 302 TGGAGATTATTACTGCTTCAAGGTCACATGTTCCCTACACGTTCCGAGGGGGACCA 361

QY 770 agctggaataaaaa 783
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Db 362 AGCTGGAATAAAAA 375

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Search completed: January 18, 2002, 00:16:31
 Job time: 1709 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2002, 00:40:07 ; Search time 43.97 Seconds

(without alignments)
453.166 Million cell updates/sec

Title: US-09-358-321c-32

Perfect score: 1391

Sequence: I MWSAIVLVLLAAAHSAFA.....FGGKLEKEKLEEDL 269

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_1101:*

1: /SIDS2/gcgdata/geneseq/AA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/AA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/AA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/AA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/AA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/AA1985.DAT:*

7: /SIDS2/gcgdata/geneseq/AA1986.DAT:*

8: /SIDS2/gcgdata/geneseq/AA1987.DAT:*

9: /SIDS2/gcgdata/geneseq/AA1988.DAT:*

10: /SIDS2/gcgdata/geneseq/AA1989.DAT:*

11: /SIDS2/gcgdata/geneseq/AA1990.DAT:*

12: /SIDS2/gcgdata/geneseq/AA1991.DAT:*

13: /SIDS2/gcgdata/geneseq/AA1992.DAT:*

14: /SIDS2/gcgdata/geneseq/AA1993.DAT:*

15: /SIDS2/gcgdata/geneseq/AA1994.DAT:*

16: /SIDS2/gcgdata/geneseq/AA1995.DAT:*

17: /SIDS2/gcgdata/geneseq/AA1996.DAT:*

18: /SIDS2/gcgdata/geneseq/AA1997.DAT:*

19: /SIDS2/gcgdata/geneseq/AA1998.DAT:*

20: /SIDS2/gcgdata/geneseq/AA1999.DAT:*

21: /SIDS2/gcgdata/geneseq/AA2000.DAT:*

22: /SIDS2/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length DB	ID	Description
1	1391	100.0	269	AA168992	Amino acid sequence
2	990	71.2	267	AA809776	TMV 30K movement p
3	984.5	70.8	274	AA823819	Plasmid psch2 MABL
4	978.5	70.3	271	AA823820	Plasmid psch2 MAB
5	963.5	69.3	274	AA823817	Plasmid psch2 MAB
6	957.5	68.8	271	AA823818	Plasmid psch2 MAB
7	944	67.9	532	AA178328	Bispecific anti-ze
8	943.5	67.8	251	AA178328	Mouse scfv fragmen
9	943.5	67.8	251	AA178328	Mouse scfv fragmen
10	927.5	66.7	252	AA178328	Mouse scfv fragmen
11	927.5	66.7	252	AA178328	Mouse scfv fragmen

RESULT	ID	Score	Query Match	Length DB	ID	Description
1	AA168992	1391	100.0	269	AA168992	Amino acid sequence of a single chain anti-delta9-desaturase antibody.
2	AA809776	990	71.2	267	AA809776	TMV 30K movement p
3	AA823819	984.5	70.8	274	AA823819	Plasmid psch2 MAB
4	AA823820	978.5	70.3	271	AA823820	Plasmid psch2 MAB
5	AA823817	963.5	69.3	274	AA823817	Plasmid psch2 MAB
6	AA823818	957.5	68.8	271	AA823818	Plasmid psch2 MAB
7	AA178328	944	67.9	532	AA178328	Bispecific anti-ze
8	AA178328	943.5	67.8	251	AA178328	Mouse scfv fragmen
9	AA178328	943.5	67.8	251	AA178328	Mouse scfv fragmen
10	AA178328	927.5	66.7	252	AA178328	Mouse scfv fragmen
11	AA178328	927.5	66.7	252	AA178328	Mouse scfv fragmen

DR N-PSDB: AAZ61047.
XX
PT Novel nucleic acid construct for down-regulating steady state levels of
PT proteins in plant cells, transgenic plants and their progeny
XX
XX Claim 22: Page 96-97; 114pp: English.
XX
CC The present sequence represents a single chain antibody which is
CC directed against a Zea mays (maize) delta9-desaturase. The sequence
CC is used to produce the constructs of the invention. These constructs
CC encode an antibody that can bind a transit peptide that directs an
CC associated passenger protein to a plant cell organelle. The transit
CC peptide sequence of the maize stearoyl-ACP-delta9-desaturase
CC (delta9-desaturase) was determined, and used to produce antibodies
CC of the invention. These antibodies were produced in transgenic plants
CC or the invention. The constructs of the invention are useful for
CC producing antibodies which decrease steady state levels of passenger
CC proteins in the organelles of plant cells and plants, by binding to
CC the transit peptide. This results in the production of transgenic
CC plants which have altered steady state passenger protein levels.
XX
SQ Sequence 269 AA;
Query Match 100.0%; Score 1391; DB 21; Length 269;
Best Local Similarity 100.0%; Pred. No. 1,9e-100;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVAIVYLVLLAAAHSAFAVQLQSGAELVRPGASVYLTSCASGYTFDYEIHWRGT 60
DB 1 mvaivlyvllaaahsaafaavgqgsgaelvrpgasvyltscasgytfdyelhwrqt 60
QY 61 PVHGLEWIGATDPTGTGAANOKFKDAIVTVKSSSTAYMELRLTSDSAVYYTTF 120
DB 61 pvhglewigatdptgtgaanokfkdaivtvkssstgmetrltssdsavyyttrf 120
QY 121 EDWGGTLVTVSAEGKSSGSESKPGDVVYTPNPLSLPYSLDQASISCRSSQSLHSN 180
DB 121 edwggtlvtvsaegekssgseekpgdvvymtpnplslpyslgdqasiscrssqslhsn 180
QY 181 GITVHWYLOKRGSPKLLTKVSNRRSGVDRPSSGSGTDTLTLSVEADLCVYFC 240
DB 181 gitvhwylqkrgspklltkvsnrrsgvdrpdtisgsgtdtltlkrveadlgyvfc 240
QY 241 SOSTHVPYTFGGGTLEIKKEKLISEEDL 269
DB 241 sqsthvpytfgggtleikeekliseedl 269
RESULT 2
AAB09776
ID AAB09776 standard; Protein: 267 AA.
AC AAB09776;
XX
DT 06-SEP-2000 (first entry)
XX
DE TMV 30k movement protein and scFv fusion protein scFv 30-2 SEQ ID NO:30.
XX
XX Molecular pathogenicide; plant disease; resistance; antibody; scFv;
XX gene construct; pathogen; toxin; fusion protein; antimicrobial;
XX deoxyribonuclease; RNase; ribosome inactivator; immunomodulator.
OS Tobacco mosaic virus.
XX
PN WO200023593-A2.
XX
PD 27-APR-2000.
XX
PF 15-OCT-1999; 99WO-EP07844.
XX
PR 16-OCT-1998; 98EP-0119630.
PR 16-OCT-1998; 98IN-0000666.

XX
PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
XX
PI Fischer R, Schillberg S, Naehring J, Sack M, Monecke M, Liao Y;
PI Spiegel H, Zimmermann S, Emans N, Holzem A;
XX
XX WPI: 2000-339692/29.
DR
XX
XX New fusion proteins and gene constructs for expressing agents
PT (antibodies, enzymes, vectors or molecular pathogenicides), useful for
PT protecting plants against pathogens and increasing resistance to
PT disease
XX
PS Example 5; Page 150-151; 193pp: English.
XX
XX The present invention describes a fusion protein (I) comprising at least
CC one binding domain specifically recognising an epitope of a plant
CC pathogen and at least one further domain comprising a protein or peptide
CC sequence which is toxic to the pathogen or detrimental to its
CC replication, transmission or life cycle. Also described is a
CC pathogenicide (II) comprising (I) and a cellular targeting sequence
CC and/or membrane localisation sequence and/or motif that leads to
CC membrane anchoring; or at least one binding domain that specifically
CC recognises a viral movement and/or replicase protein. The fusion
CC protein, pathogenicide, polynucleotide, vectors, and compositions from
CC the present invention are useful for the protection of a plant against
CC the action of a pathogen. The kit from the present invention is useful
CC for carrying out the methods and may be employed in different
CC applications, for example in the diagnostic field or as research tools.
CC The kit or its components, such as the fusion protein, pathogenicide,
CC polynucleotides, vectors or compositions are useful in plant cell and
CC plant tissue culture, in agriculture. They are extremely useful for
CC breeding new varieties of plants that display improved properties such as
CC resistance to pathogens. AAs5687 to AAs5702 and AAB09774 to B097820
CC represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 267 AA;
Query Match 71.2%; Score 990; DB 21; Length 267;
Best Local Similarity 74.4%; Pred. No. 2,5e-69;
Matches 195; Conservative 21; Mismatches 32; Indels 14; Gaps 3;
QY 22 VOLQSGAELVRPGASVYLTSCASGYTFDYEIHWRQTPVHGLEWIGATDPTGTAYN 81
DB 2 vqlqsgaelvrpgasvyltscasgytfdyelhwrqtpvhglewigatdptgtayn 81
QY 82 OKFKDAIVTVKSSSTAYMELRLTSDSAVYY-----YTRWEDMGCGTLTVVSAEG 135
DB 82 okfkdaivtvkssstaymrltssdsavyy-----ytrwfdmgcgtltvvsag 135
QY 136 KSSGSGSESKPG-DVWTPNPLSLPYSLDQASISCRSSQSLHSNGITVLYLHWYLOKRGQ 194
DB 136 kssgsgsekspg-dvwtppnplslpyslgdqasiscrssqslhsngitvlylhwylorkrgq 194
QY 195 SPKLLTKVSNRRSGVDRPSSGSGTDTLTLSRLEADLCVYFCOSTHVPYTFGGGT 254
DB 195 spklltkvsnrrsgvdrpssgsgtdtltlsrleadlcvyfcosthvpvtfgggt 254
QY 255 KLEIK-----EKKLISEEDL 269
DB 255 kleik-----ekliseedl 269
RESULT 3
AAB23819
ID AAB23819 standard; Protein: 274 AA.
XX
AC AAB23819;
XX
DT 15-JAN-2001 (first entry)
XX

DE Plasmid pSCM2 MABL2-scFv protein sequence SEQ ID NO:24.
 XX
 XX Monoclonal antibody; MABL; IAP; integrin associated protein;
 KW single stranded Fv; apoptosis; blood disease; leukaemia;
 KW cyostatic.
 XX
 XX Mus sp.
 OS
 XX WO200053634-A1.
 PN
 XX 14-SEP-2000.
 PD
 XX 10-MAR-2000; 2000MO-JP01458.
 PE
 XX 10-MAR-1999; 99JP-0063557.
 PR
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA
 XX Fukushima N, Uno S;
 PI
 XX WPI: 2000-587428/55.
 DR
 XX N-PSDB; AAA92443.
 DR
 XX
 PT Single stranded Fv antibody fragment inducing apoptosis in nucleated
 PT blood cells having integrin associated protein for treatment of
 PT leukemia -
 XX
 XX Example 5; Page 64-66; 73pp; Japanese.
 PS
 XX
 CC The present invention describes a polypeptide containing the variable
 CC region of the light chain of a monoclonal antibody, which induces
 CC apoptosis in nucleated blood cells having integrin associate protein
 CC (IAP). Also described are: (1) DNA encoding the novel polypeptide;
 CC (2) animal or microbial cells expressing the DNA of (1); and (3) agents
 CC for the treatment of blood disorders which contain the polypeptide.
 CC The polypeptide can be used in the treatment of blood disorders such
 CC as leukaemia. The present sequence represents the protein sequence from
 CC pSCM2 MABL2-scFv, which is used in an example from the present
 CC invention.
 CC
 XX
 XX Sequence 274 AA;
 SQ

Query Match 70.8%; Score 984.5; DB 21; Length 274;
 Best Local Similarity 76.0%; Pred. No. 7e-69;
 Matches 196; Conservative 16; Mismatches 41; Indels 5; Gaps 2;

QY 10 LLAHAHSAFAAVQLOQSGAELVPRGASVTLSCKASGYTFTDYEIHVROTQVHGLEWIG 69
 DB 12 LLLAAGPAMAGVGLQGSGPELVKPGASVXKMSCKASGYTFanhhvkvkpgqglewlg 71
 QY 70 AIDPETGATAYNOKFKDAIVTDKSSSTAYMELRSLTSEDSAVYYTR----WPEDMQG 125
 DB 72 YIYPNDGTLKYNEKFKDAITLSDKSETAYMDLSLASEDSAVYYCARGYTYDQWQG 131
 QY 126 GTLVVSAEGRSSSGSGSESKPG-DVWMTPNPLSLPVSLDQASISCRSSQSLHNSGITY 184
 DB 132 GTLLVSSGSGSGSGSGSDVMTGSPSLIPVSLGDDASISCRSSQSLVHNSGITY 191
 QY 189 LHWYLOKPGOSPKILLIYVSNRFGVPRFSGSGSGTDFTLKISRVAEADLGYVFCGSOST 244
 DB 192 LHWYLGKPGSPKILLIYVSNRFGVPRFSGSGSGTDFTLKISRVAEADLGYVFCGSOST 251
 QY 245 HWYTFGGGTGLKEIKEEK 262
 DB 252 HWYTFGGGTGLKEIKDYK 269

RESULT 4
 AAB23820
 ID AAB23820 standard; Protein: 271 AA.
 XX
 AC AAB23820;

XX 15-JAN-2001 (first entry)
 DT
 XX Plasmid pCHOM2 MABL2-scFv protein sequence SEQ ID NO:25.
 DE
 XX Monoclonal antibody; MABL; IAP; integrin associated protein;
 KW single stranded Fv; apoptosis; blood disease; leukaemia;
 KW cyostatic.
 XX
 XX Mus sp.
 OS
 XX WO200053634-A1.
 PN
 XX 14-SEP-2000.
 PD
 XX 10-MAR-2000; 2000MO-JP01458.
 PE
 XX 10-MAR-1999; 99JP-0063557.
 PR
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA
 XX Fukushima N, Uno S;
 PI
 XX WPI: 2000-587428/55.
 DR
 XX N-PSDB; AAA92444.
 DR
 XX
 PT Single stranded Fv antibody fragment inducing apoptosis in nucleated
 PT blood cells having integrin associated protein for treatment of
 PT leukemia -
 XX
 XX Example 5; Page 66-68; 73pp; Japanese.
 PS
 XX
 CC The present invention describes a polypeptide containing the variable
 CC region of the light chain of a monoclonal antibody, which induces
 CC apoptosis in nucleated blood cells having integrin associate protein
 CC (IAP). Also described are: (1) DNA encoding the novel polypeptide;
 CC (2) animal or microbial cells expressing the DNA of (1); and (3) agents
 CC for the treatment of blood disorders which contain the polypeptide.
 CC The polypeptide can be used in the treatment of blood disorders such
 CC as leukaemia. The present sequence represents the protein sequence from
 CC pCHOM2 MABL2-scFv, which is used in an example from the present
 CC invention.
 CC
 XX
 XX Sequence 271 AA;
 SQ

Query Match 70.3%; Score 978.5; DB 21; Length 271;
 Best Local Similarity 74.0%; Pred. No. 2e-68;
 Matches 196; Conservative 19; Mismatches 43; Indels 7; Gaps 3;

QY 3 SAIVLYVLLAAHSAFAAVQLOQSGAELVPRGASVTLSCKASGYTFTDYEIHVROTQV 62
 DB 4 scilf--lvalatgvdsgvqlqgsgpelvkvpgasvXKMSCKASGYTFanhhvkvkpg 61
 QY 63 HGLEWIGRIDETGATAYNOKFKDAIVTDKSSSTAYMELRSLTSEDSAVYYTR----- 118
 DB 62 qglewlgYIYPNDGTLKYNEKFKDAITLSDKSETAYMDLSLASEDSAVYYCARGYTY 121
 QY 119 WPEDMQGTGLVSAEGRSSSGSGSESKPG-DVWMTPNPLSLPVSLDQASISCRSSQSL 177
 DB 122 TYDQWQGTLTLVSSGSGSGSGSGSDVMTGSPSLIPVSLGDDASISCRSSQSLV 181
 QY 178 HNSGITYLHWYLOKPGOSPKILLIYVSNRFGVPRFSGSGSGTDFTLKISRVAEADLGY 237
 DB 182 HNSGITYLHWYLGKPGSPKILLIYVSNRFGVPRFSGSGSGTDFTLKISRVAEADLGY 241
 QY 238 YFCGSOSTHWYTFGGGTGLKEIKEEK 262
 DB 242 YFCGSOSTHWYTFGGGTGLKEIKDYK 266

RESULT 5
 AAB23817

ID AAB23817 standard; Protein; 274 AA.
XX
AC AAB23817;
XX
DT 15-JAN-2001 (first entry)
XX
DE Plasmid pCHO1 MAB1-scFv protein sequence SEQ ID NO:20.
XX
KW Monoclonal antibody; MAB1; IAP; integrin associated protein;
KW single stranded Fv; apoptosis; blood disease; leukemia;
KW cytosolic.
XX
OS Mus sp.
XX
PN WO200053634-A1.
XX
PD 14-SEP-2000.
XX
PF 10-MAR-2000; 2000WO-JP01458.
XX
PR 10-MAR-1999; 99JP-0063557.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Fukushima N, Uno S;
XX
DR WPI: 2000-587428/55.
DR N-PSDB: AAA92439.
XX
XX
PT Single stranded Fv antibody fragment inducing apoptosis in nucleated
PT blood cells having integrin associated protein for treatment of
PT leukemia
XX
PS Example 5; Page 59-61; 73pp; Japanese.
XX
CC The present invention describes a polypeptide containing the variable
CC region of the light chain of a monoclonal antibody, which induces
CC apoptosis in nucleated blood cells having integrin associate protein
CC (IAP). Also described are: (1) DNA encoding the novel polypeptide;
CC (2) animal or microbial cells expressing the DNA of (1); and (3) agents
CC for the treatment of blood disorders which contain the polypeptide.
CC The polypeptide can be used in the treatment of blood disorders such
CC as leukemia. The present sequence represents the protein sequence from
CC pCHO1 MAB1-scFv, which is used in an example from the present
CC invention.
XX
SQ Sequence 274 AA;

Query Match 69.3%; Score 963.5; DB 21; Length 274;
Best Local Similarity 74.8%; Pred. No. 3e-67;
Matches 193; Conservative 15; Mismatches 45; Indels 5; Gaps 2;
QY 10 LLAHAHSAFAAVALQOQSGAEIVRPGASVTLSCASGTYPTDEIHMVKQTPVHGLEMIG 69
DB 12 LLLlaagmamqvgqlqsgspdlvkpgasvkmckasgytlvnhvmhwqkpgqglwlg 71
QY 70 AIDPTGCTAVNOKFKDKAIVTVDKSSSTAYMELSLTSDSAVYYTRM---FEDWQO 125
DB 72 ylypyndgtkynekfkqkatltsekssaaaymelssasedsavycargyyxyddwqg 131
QY 126 GTLVVSAEKKSSGSGSEKPG-DVYMTNPPLSLPVSLGPOASISCRSSQSLHSHSGITY 184
DB 132 gtltlvssggsg 191
QY 185 LHWLQKPGQSPKLLITKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCQSQT 244
DB 192 lqwydqkpgqspklllyvsnrfsydpdrfsgsgsgtdftlkisrveadlgyfcsqgt 251
QY 245 HWPYTFGGGTLEIKEEK 262
DB 252 hwpylssgggtkltdkdx 269

RESULT 6
ID AAB23818 standard; Protein; 271 AA.
XX
AC AAB23818;
XX
DT 15-JAN-2001 (first entry)
XX
DE Plasmid pCHO1 MAB1-scFv protein sequence SEQ ID NO:23.
XX
KW Monoclonal antibody; MAB1; IAP; integrin associated protein;
KW single stranded Fv; apoptosis; blood disease; leukemia;
KW cytosolic.
XX
OS Mus sp.
XX
PN WO200053634-A1.
XX
PD 14-SEP-2000.
XX
PF 10-MAR-2000; 2000WO-JP01458.
XX
PR 10-MAR-1999; 99JP-0063557.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Fukushima N, Uno S;
XX
DR WPI: 2000-587428/55.
DR N-PSDB: AAA92442.
XX
XX
PT Single stranded Fv antibody fragment inducing apoptosis in nucleated
PT blood cells having integrin associated protein for treatment of
PT leukemia
XX
PS Example 5; Page 62-64; 73pp; Japanese.
XX
CC The present invention describes a polypeptide containing the variable
CC region of the light chain of a monoclonal antibody, which induces
CC apoptosis in nucleated blood cells having integrin associate protein
CC (IAP). Also described are: (1) DNA encoding the novel polypeptide;
CC (2) animal or microbial cells expressing the DNA of (1); and (3) agents
CC for the treatment of blood disorders which contain the polypeptide.
CC The polypeptide can be used in the treatment of blood disorders such
CC as leukemia. The present sequence represents the protein sequence from
CC pCHO1 MAB1-scFv, which is used in an example from the present
CC invention.
XX
SQ Sequence 271 AA;

Query Match 68.8%; Score 957.5; DB 21; Length 271;
Best Local Similarity 72.8%; Pred. No. 8.6e-67;
Matches 193; Conservative 18; Mismatches 47; Indels 7; Gaps 3;
QY 3 SAIVLYVLLAAHSAFAAVALQOQSGAEIVRPGASVTLSCASGTYPTDEIHMVKQTPV 62
DB 4 scilf--lvatalgyvsgvgqlqsgspdlvkpgasvkmckasgytlvnhvmhwkpgq 61
QY 63 HGLEWGAIDPTGCTAVNOKFKDKAIVTVDKSSSTAYMELSLTSDSAVYYTRM--- 119
DB 62 gglwliwlylpyndgtkynekfkqkatltsekssaaaymelssasedsavycargyy 121
QY 120 -FEDWQOGLTVVSAEKKSSGSGSEKPG-DVYMTNPPLSLPVSLGPOASISCRSSQSL 177
DB 122 syddwgggtltlvssggsgsgsgsgsgsgsgsgsgsgsgsgsgsgsgsgsgsgsg 181
QY 178 HSNGITLHWYLOKPGQSPKLLITKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGV 237
DB 182 hskgnilylqwydqkpgqspklllyvsnrfsydpdrfsgsgsgtdftlkisrveadlgy 241
QY 238 YFCSQSTHWPYTFGGGTLEIKEEK 262


```

XX  US5837846-A.
XX
XX  17-NOV-1998.
XX
XX  05-JUN-1995; 95US-0461386.
XX
XX  07-OCT-1993; 93US-0133804.
XX  06-FEB-1992; 92US-0831967.
XX  05-JUN-1993; 95US-0461386.
XX
XX  (CHIR ) CHIRON CORP.
XX  (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX  Houston LL, Huston JS, Oppermann H, Ring DB;
XX
XX  WPI: 1999-023541/02.
XX  N-PSDB; AAV63398.
XX
XX  Nucleic acid encoding single-chain Fv fragment specific for antigens
XX  - and having C-terminal tail for crosslinking to form dimer with
XX  improved pharmacokinetic properties, used to deliver drugs and
XX  imaging agents, especially to tumours
XX
XX  Example 1; Columns 31-34; 29pp; English.
XX
XX  The present sequence represents an anti-digoxin sfv'. Antibody 26-10
XX  binds digoxin. The present sequence exemplifies the invention.
XX  CC  Dimers of the single chain Fv are used for targeted delivery of
XX  CC  drugs or imaging agents (e.g. cytotoxins, prodrugs or 99m-technetium)
XX  CC  to antigen-expressing cells, particularly for treatment or diagnosis
XX  CC  of tumours (especially of ovary or breast).
XX
XX  Sequence 252 AA:
XX
XX  Query Match 56.7%; Score 927.5; DB 20; Length 252;
XX  Best Local Similarity 76.6%; Pred. No. 1.7e-64;
XX  Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps 3;
XX
XX  QY 22 VOLOSGAEIYRPGASVTLSCKASGYFTDYEHMWQPTVHGLEWIGALDPEGTAYN 81
XX  DB 3 VQIQSGPELVKPGASVYRMCKSSGYLFTDLYNMWVRQSHGKSLDYIYISPYSGVLTGM 62
XX
XX  QY 82 QKFKDAIVTDKSSSTAYMELRSLTSEDSAVYYY----TRWFED-WQOGTLVTVSAG 135
XX  DB 63 QKfkgkaltlvdkssstajmeltstedsavyycaqsgnkwamdywbgasvltvssg 122
XX
XX  QY 136 KSSGSGESKRGDYYMTNPPLSLPVSLGDDASISCRSSQSLNSNGITLYLHWLQKPGQS 195
XX  DB 123 -sssgsssssgsdvmtcqlpisljpvslgddasiscrssgslvhsngnlylnwylqkaqgs 181
XX
XX  QY 186 PRLIYKYNRFGVPPDRFSGSGSGTDFTLKISRVEAEDYGVYFCQSTHVPYTFEGGTR 255
XX  DB 182 PKLLIYKYNRFGVPPDRFSGSGSGTDFTLKISRVEAEDYGVYFCQSTHVPYTFEGGTR 241
XX
XX  QY 256 LEIK 259
XX  DB 242 Ieik 245
XX
XX  RESULT 13
XX  AAR27244
XX  ID AAR27244 standard; Protein; 367 AA.
XX
XX  AAR27244;
XX
XX  25-FEB-1993 (first entry)
XX
XX  Sequence encoded by the MLE-mFB-sfv gene in plasmid pH912.
XX
XX  Fusion protein; serine-rich peptide linker; protease resistant.
XX

```

```

OS  Synthetic.
XX
XX  Key Location/Qualifiers
XX  FT Protein 1..59
XX  FT Protein /label= modified trp LE leader peptide
XX  FT Protein 61..121
XX  FT Protein /label= modified fragment B
XX  FT Protein /note="Of Staphylococcal protein A"
XX
XX  W09215682-A.
XX
XX  17-SEP-1992.
XX
XX  27-FEB-1992; 92MO-US01478.
XX  27-FEB-1991; 91US-0662226.
XX
XX  (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX  Huston JS, Oppermann H, Timasheff SN;
XX
XX  WPI: 1992-331728/40.
XX  N-PSDB; AAQ28572.
XX
XX  Fusion proteins comprising serine-rich peptide linkers - have
XX  PT improved solubility in physiological media, resistance to
XX  PT proteolysis and enhanced regolding properties.
XX
XX  Example; pages 30-32; 49pp; English.
XX
XX  AAR27243 is a prefd. linker of the invention. The advantage of such
XX  CC linkers is that they can improve the refolding properties of the
XX  CC fusion protein expressed in procarotes. The linker itself is
XX  CC resistant to proteolysis. In particular it is used to fuse domains
XX  CC mimicking vH and vL from monoclonal antibody, to produce single
XX  CC chain binding site proteins (sfv) which dissolve in physiological
XX  CC media, retain their activity at high concentrations, and resist
XX  CC lysis by endogenous proteases. pH912 was pred. in order to
XX  CC evaluate an anti-digoxin 26-10 sfv contg. a Ser-rich peptide
XX  CC linker.
XX
XX  Sequence 367 AA:
XX
XX  Query Match 66.5%; Score 925.5; DB 13; Length 367;
XX  Best Local Similarity 74.3%; Pred. No. 3.8e-64;
XX  Matches 188; Conservative 19; Mismatches 39; Indels 7; Gaps 3;
XX
XX  QY 13 AAASATAAVQLOSGAEIYRPGASVTLSCKASGYFTDYEHMWQPTVHGLEWIGALD 72
XX  DB 115 aqabksdpvqqlqsgpelvKpgasvrmckssgyLFTDLYNMWVRQSHGKSLDYIYIS 174
XX
XX  QY 73 PETGTAIYNOKFKKDAIVTDKSSSTAYMELRSLTSEDSAVYYY----TRWFED-WQOG 126
XX  DB 175 psgvtlyngdkfkgtaltlvdkssstajmeltstedsavyycaqsgnkwamdywbg 234
XX
XX  QY 127 TLVTVAEGRKSSGSGSKRGDYYMTNPPLSLPVSLGDDASISCRSSQSLNSNGITLYLH 186
XX  DB 235 asvltvsssg-sssgsssssgsdvmtcqlpisljpvslgddasiscrssgslvhsngnlyln 293
XX
XX  QY 187 WYLOKPGQSPKRLIYKYNRFGVPPDRFSGSGSGTDFTLKISRVEAEDYGVYFCQSTHVP 246
XX  DB 294 wylqkaqgsPKLLIYKYNRFGVPPDRFSGSGSGTDFTLKISRVEAEDYGVYFCQSTHVP 353
XX
XX  QY 247 PYTFGGGTKLEIK 259
XX  DB 354 pPtfggggtkIeik 366
XX
XX  RESULT 14
XX  AAP80154
XX  ID AAP80154 standard; Protein; 249 AA.
XX

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AC AAP80154;
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	Query Match	66.4%	Score 923.5	DB 9	Length 249
	Best Local Similarity	74.9%	Pred. NO. 3.4e-64		
	Matches 182; Conservative	18;	Mismatches 38;	Indels 5;	Gaps 2
QY	22	VVLQOAGAEIVRGASAVTLSCAKSGYTFPIIDYIEHVRQTPPHGEMICATLDPETGGAYN	81		
Dd	4	vqlqgspeplvhpqgasvrmscksgyglfnyihulkshngsklewjwlylpgnqnkknn	63		
QY	82	QKEFDKAIIVTVDKSSSTATWELSLTSEDSAAVYYTR---WFEDWGCGITLVTSABEGKS	137		
Dd	64	enifgkcltlvdksstslaymelrsltsedaaavycaeyrlhyfyfdwqhgasaavltvsqg99	133		
QY	138	SGSGSESEKRp-DVVMPPNPILSPVLSGLDDASISCRSSOSLHNSGNITVLMHYLDKPCOSP	196		
Dd	124	sg9gsgsg99gdvrmcqtprlsipvalsqdasiscrsqsqlivhmgnylwyldkagqsp	163		
QY	197	KLLIKYSNFSGVPAPRFGSGSGCMPTLIKIRVAEQLGVFPQSQRHHVYTPRGSGTKL	256		
Dd	184	klllykrsmnfisypatfisssgsqctfltklsirveaalglyclfgshvpwtlrg9xtkl	243		
QY	257	EIK 259			

```

Db      244 eik 246

RESULT 15
ID      AAR27245
AC      AAR27245 standard; Protein; 246 AA.
XX
XX      AAR27245:
XX
XX      25-FEB-1993 (first entry)
XX
XX      Sequence of the AA sequences mimicking the light (VL) and
XX      heavy (VH) chain variable regions of an antibody linked to Jform a
XX      single chain antibody binding site (sfv).
XX
XX      Fusion protein; serine-rich peptide linker; protease resistant.
XX
XX      Synthetic.
XX
XX      Key
XX      Domain
XX      Region
XX      Domain
XX      WO9215682-A.
XX      17-SEP-1992.
XX      27-FEB-1992; 92WO-US01478.
XX      27-FEB-1991; 91US-0662226.
XX      (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX      Huston JS, Oppermann H, Timasheff SN;
XX      WPI; 1992-311728/40.
XX      DR      N-PSDB; AAC28573.
XX
XX      Fusion proteins comprising serine-rich peptide linkers - have
XX      improved solubility in physiological media, resistance to
XX      proteolysis and enhanced regolding properties.
XX
XX      Example; pages 34-35; 49pp; English.
XX
XX      AAR27243 is a pref. linker of the invention. The advantage of such
XX      linkers is that they can improve the refolding properties of the
XX      fusion protein expressed in procarcytes. The linker itself is
XX      resistant to proteolysis. In particular it is used to fuse domains
XX      mimicking VH and VI from monoclonal antibody, to produce single
XX      chain binding site proteins (sfv) which dissolve in physiological
XX      media, retain their activity at high concentrations, and resist
XX      lysis by endogenous processes. pH912 was pred. in order to
XX      evaluate an anti-digoxin 26-10 sfv contg. a Ser-rich peptide
XX      linker.
XX
XX      Sequence 246 AA:

Query Match 66.3%; Score 922.5; DB 13; Length 246;
Best Local Similarity 76.2%; Pred. No 4e-64;
Matches 186; Conservative 17; Mismatches 34; Indels 7; Gaps 3;

22 VQLQSGCAELVPRGASVLTSCRKASGYTFTEDEIHWVROQYHGLEWIGALDPTGTAVN 81
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3 vqlqhsgepelvkvpgasvrmscksgyiftdfymwvrgsbqskidlygyispygytlgn 62

82 QREKDAIIVYVCKSSSTAYMELRSLTSDSAVYYY-----TRFED-WGGGLIYVYSAAG 135
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
63 qkltgkaltlvdcssstlaymelrsltsedsavyyccagsgnkvamdywqhgasvltvssg 122

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QY 136 KSSGSGSESKPGDVVMTPNPLSLPVSJGDOASISCRSSOSLHSHNGITYLHMYLQKPGOS 195
Db 123 -ssssgsssgsdvymLqPpLslpvsLgddasiscrssqslvhsngtlylnwyLqkagqs 181
QY 196 PKLLIYKVSNNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVFCSSQSTHVPYTFGGGTR 255
Db 182 PKLLIYKVSNNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVFCSSQSTHVPYTFGGGTR 241
QY 256 LEIK 259
Db 242 LEIK 245

Search completed: January 18, 2002, 01:23:47
Job time: 2620 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2002, 00:41:18 ; Search time 26.93 Seconds

(without alignments)
224.782 Million cell updates/sec

Title: US-09-358-321C-32

Perfect score: 1391
Sequence: 1 MVSALVLYVLLAAAHSAFA.....FGGOTKLEIKERLISEEDL 269

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
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5: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the total being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	928.5	66.8	367	1	US-08-257-341-5	Sequence 5, Appli	
	2	927.5	66.7	246	1	US-08-257-341-7	Sequence 7, Appli	
	3	927.5	66.7	252	1	US-08-133-804-4	Sequence 4, Appli	
	4	927.5	66.7	252	1	US-08-461-838-4	Sequence 4, Appli	
	5	927.5	66.7	252	2	US-08-461-886-4	Sequence 4, Appli	
	6	848.5	61.0	269	4	US-09-070-408-132	Sequence 132, App	
	7	818.5	58.8	260	2	US-08-447-402-1	Sequence 1, Appli	
	8	806.5	58.0	247	4	US-09-227-693-34	Sequence 34, Appli	
	9	806.5	58.0	248	1	US-08-331-398A-34	Sequence 34, Appli	
	10	806.5	58.0	248	2	US-08-331-397B-34	Sequence 34, Appli	
	11	806.5	58.0	248	2	US-08-759-804A-34	Sequence 34, Appli	
	12	788.5	56.7	638	4	US-09-070-637-20	Sequence 20, Appli	
	13	767	55.1	273	2	US-08-403-853-18	Sequence 18, Appli	
	14	762	54.8	365	3	US-08-875-811-53	Sequence 53, Appli	
	15	762	54.8	366	3	US-08-875-811-55	Sequence 53, Appli	
	16	761.5	54.7	281	4	US-09-025-769B-17	Sequence 17, Appli	
	17	761	54.7	271	2	US-08-894-922A-10	Sequence 10, Appli	
	18	755.5	54.3	263	2	US-08-752-844-66	Sequence 66, Appli	
	19	747	53.7	252	2	US-08-894-922A-14	Sequence 14, Appli	
	20	742	53.3	239	3	US-08-279-772A-8	Sequence 8, Appli	
	21	742	53.3	239	4	US-08-902-486-11	Sequence 11, Appli	
	22	741	53.3	553	2	US-08-263-911-7	Sequence 7, Appli	
	23	740.5	53.2	483	2	US-08-392-338A-19	Sequence 19, Appli	
	24	740.5	53.2	483	3	US-09-166-750-19	Sequence 19, Appli	
	25	740.5	53.2	483	3	US-09-166-093-19	Sequence 19, Appli	
	26	740.5	53.2	483	3	US-09-172-019-19	Sequence 19, Appli	
	27	740.5	53.2	483	3	US-09-166-094-19	Sequence 19, Appli	

28	740	53.2	553	2	US-08-263-911-9	Sequence 9, Appli
29	739	53.1	289	3	US-09-184-658-63	Sequence 63, Appli
30	739	53.1	599	1	US-08-463-163-3	Sequence 3, Appli
31	728.5	52.4	244	2	US-08-553-497A-20	Sequence 20, Appli
32	726.5	52.2	246	2	US-08-553-497A-24	Sequence 24, Appli
33	718	51.6	246	1	US-08-469-486-57	Sequence 57, Appli
34	718	51.6	246	2	US-08-469-486-57	Sequence 57, Appli
35	713.5	51.3	244	2	US-08-553-497A-22	Sequence 22, Appli
36	709.5	51.0	242	2	US-08-553-497A-26	Sequence 26, Appli
37	705	50.7	282	2	US-08-860-174A-10	Sequence 10, Appli
38	698.5	50.2	242	2	US-08-553-497A-28	Sequence 28, Appli
39	696.5	50.1	637	1	US-08-232-838-16	Sequence 16, Appli
40	696.5	50.1	637	2	US-08-465-473B-16	Sequence 16, Appli
41	693	49.8	553	2	US-08-661-052-16	Sequence 16, Appli
42	693	49.8	553	4	US-09-188-082-16	Sequence 16, Appli
43	689	49.5	240	2	US-08-800-198-8	Sequence 8, Appli
44	689	49.5	240	3	US-09-296-595-8	Sequence 8, Appli
45	688	49.5	270	2	US-08-652-507-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-257-341-5
Sequence 5, Application US/08257341
Patent No. 5525491
GENERAL INFORMATION:
APPLICANT: HUSTON, JAMES S
APPLICANT: OPPERMAN, HERMANN
APPLICANT: TIMASHEFF, SERGE N
TITLE OF INVENTION: SERINE RICH PEPTIDE LINKER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
STREET: 35 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,341
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/842,149
FILING DATE:
APPLICATION NUMBER: US 07/662,226
FILING DATE: 27-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, ESQ, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: CRP-064CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000 (ATTY)
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-257-341-5

Query Match 66.8%; Score 928.5; DB 1; Length 367;
Best Local Similarity 74.7%; Pred. No. 7.7e-80;
Matches 189; Conservative 18; Mismatches 39; Indels 7; Gaps 3;

Db	63	QKFKGKATLTVDKSSSTAYAMELRSLTPEDSAVYYCAGSGSGNKKMADYNGHGASVYVSSG	122
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	123	-SSSSSSSSSGSDYVMTQTPRLSPVSLGGDASTISCRSSQSLVHNSGNTLYLHWYLQKAGQS	181
QY	196	PKLLIKVSNRRSGVPODRFSSGSGDTFLKISRVAEDLGVPFCSQSTHWPIYFGGATK	255
Db	182	PKLLIKVSNRRSGVPODRFSSGSGDTFLTKISRVAEDLGVPFCSQSTHWPIYFGGATK	241
QY	256	LEIK	259
Db	242	LEIK	245

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1      RESULT      4
2      US-08-461-838-4
3      : Sequence 4, Application US/08461838
4      : Patent No. 5753204
5      : GENERAL INFORMATION:
6      : APPLICANT: Huston, James S.
7      : APPLICANT: Oppermann, Hermann
8      : APPLICANT: Houston, L. L.
9      : APPLICANT: Ring, David B.
10     : TITLE OF INVENTION: Biosynthetic Binding Proteins For
11     : TITLE OF INVENTION: Imaging
12     : NUMBER OF SEQUENCES: 11
13     : CORRESPONDENCE ADDRESS:
14     : ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
15     : STREET: Exchange Place, 53 State Street
16     : CITY: Boston
17     : STATE: Massachusetts
18     : COUNTRY: USA
19     : ZIP: 02109
20     : COMPUTER READABLE FORM:
21     : MEDIUM TYPE: Floppy disk
22     : COMPUTER: IBM PC compatible
23     : OPERATING SYSTEM: PC-DOS/MS-DOS
24     : SOFTWARE: Patent Release #1.0, Version #1.25
25     : CURRENT APPLICATION DATA:
26     : APPLICATION NUMBER: US/08/461,838
27     : FILING DATE:
28     : CLASSIFICATION: 424
29     : ATTORNEY/AGENT INFORMATION:
30     : NAME: Kelley, Robin D.
31     : REGISTRATION NUMBER: 34,637
32     : REFERENCE/DOCKET NUMBER: 2054/22
33     : TELECOMMUNICATION INFORMATION:
34     : TELEPHONE: 617-248-7477
35     : TELEFAX: 617-248-7100
36     : INFORMATION FOR SEQ ID NO: 4:
37     : SEQUENCE CHARACTERISTICS:
38     : LENGTH: 252 amino acids
39     : TYPE: amino acid
40     : TOPOLOGY: linear
41     : MOLECULE TYPE: protein
42     : OS-08-461-838-4

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Query Match: 65.7%; Score 927.5; DB 1, Length 252;
 Best Local Similarity 76.6%; Pred. No. 5.7e-80;
 Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps 3.

[illegible]

```

RESULT 5
US-08-461-386-4
Sequence 4, Application US/08461386
Patent No. 5837846
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
City: Boston
STATE: Massachusetts
COUNTRY: USA
Zip: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461.386
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-386-4

```

Query Match	65-78:	Score	927.5:	DB	2:	Length	252:
Best Local Similarity	75.6%:	Pred	No. 5.7e-80:				
Matches	187:	Conservative	17:	Mismatches	33:	Indels	7:
							Gaps
							3:
QY	22	VQLDQSGAEILVPRGASVLTSCASGAGYTTTDEIHWVROTPLYGLMIGALIDPETGTAYN	81				
Db	3	VQLDQSGPELPLVYKGAASVRMSCKSSGIFTDPMVMVVRQSHGKSLDYIGYISPLPSGVTGVN	62				
QY	82	QKFKDAIIVLDKSSSTAYMELRLSTSEDSAYYYY-----TRWPEL-WGQGTLYTVSAEG	135				
Db	63	QKFKGKATLLVDRKSSSTAYMELRLSTSEDSAYVYCAAGSSGNKAMDYVGHGASVATYSSSG	122				
QY	136	KSSGSGSEKRPQVYWTPLPLSLPSLDQASISCRSSQSLHNGTITLHWLQKPGQS	195				
Db	123	-SSSSGSSSSGSLVMTQTPLSLPLSLGQASISCRSSQSLVHSHNGTITLHWLQKRAQGS	181				
QY	196	PKLLIYKVSNRFSGVDRFSGSGSTDFLKLISRYEAEDLGVFCQSSTHVPYTFGGGTR	255				

Db 182 PKLLIKVNSRSGVPDRFSSGSGSTFDLIKISHVEADLDGIFCSQTTHTPPITFGGSK 241

Qy 256 LEIK 259
|||

Db 242 LEIK 245

RESULT 6
US-09-070-408-132

Query Match	61.0%;	Score 848.5;	DB 4;	Length 269;
Best Local Similarity	69.7%;	Pred. No. 1.8e-72;		
Matches 170; Conservative	23;	Mismatches 44;	Indels 7;	Gaps 3

QY	255	KLEI	258
Db	243	KLEI	246

RESULT 7
US-08-447-402-1
; Sequence 1, Application US/08447402

Query Match	58.8%;	Score 818.5;	DB 2;	Length 260;
Best Local Similarity	66.9%;	Pred. No. 1.2e-69;		
Matches 164;	Conservative 26;	Mismatches 48;	Indels 7;	Gaps 3

```

Oy 22 VLODQSSAEVLVRGASAVITLSCASSYTTDEIHWFOQPHLEWIGADIBETGQXVYN 81
Db 3 VKLWSSGGGLVYGSGSLKASCATSGFTFSDYVWVWQPERKLEWAVIINSDSSAVS 62
Oy 82 QKFDKAIYVNDSSSTAMELRSLTSDSAVYYTFR-----WEDMQGGLVLYVSAEG 133
Db 63 DYVAGRTTIRDNARNTLTLLQWSRLKSDTLVYSCAGLAWGAMPFVWQGLVLYVSSGG 122

```

Oy 22 VOLOSGAEILVRGCAVTLTSCASQAYTFPDEIHWRQTPEHGLEMGALDPEITGNAYN 81
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 3 VKLWSSGGGLVQGGSGLKUSCATSGFTSDYIMMYRQTPPKRLKLEMAIYISNDSSAAYS 62

Best Local Similarity 63.7%; Pred. No. 1.95-66;
Matches 156; Conservative 29; Mismatches 53; Indels 7; Gaps

QY	QKRDKAITYVKKSSSTAYMEARJSTEDSAVYYTR-----WEDMGOGGLTVYSNEG	135
Db	63 DYVKGFTTISRDNAKNTILYLQMSRLKSEDAITATSCARGLAMGAMFAIKMOGLTVYVSSGC	122
QY	136 KSSGSGSESKPG-DYVWTPNPPLSLPVSILGDOASISCRSSQSLHSHNGITLYLHWYLQKPEQ	194
Db	123 GSGSGSGSGSGGSDVLTAKMGPPLSLPVSILGDOASISCRSSQIYHSHNGNTLYEWLYQKRGQ	182
QY	195 SPKLLIKYKSNRFSGVPRFSGSGSGIDFTLKISRVAEDDLGYVPCSGSTHYPTFFGGGT	254
Db	183 SPKLLIKYKSNRFSGVPRFSGSGSGIDFTLKISRVAEDDLGYVCCFGSHVPTFFGSGT	242
QY	255 KLEIK 259	
Db	243 KLEIK 247	

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10 RESULT
11 US-08-331-397B-34
12 Sequence 34, Application US/08331397B
13 Patent No. 5981726
14 GENERAL INFORMATION:
15 APPLICANT: Pastan, Ira
16 APPLICANT: Benhar, Itai
17 TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
18 TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
19 TITLE OF INVENTION: Thereof
20 NUMBER OF SEQUENCES: 68
21 CORRESPONDENCE ADDRESS:
22 ADDRESSEE: Townsend and Townsend and Crew
23 STREET: One Market Plaza, Stewart Street Plaza
24 CITY: San Francisco
25 STATE: California
26 COUNTRY: USA
27 ZIP: 94105-1492
28 COMPUTER READABLE FORM:
29 MEDIUM TYPE: Floppy disk
30 COMPUTER: IBM PC compatible
31 OPERATING SYSTEM: PC-DOS/MS-DOS
32 SOFTWARE: Patentln Release #1.0, Version #1.30
33 CURRENT APPLICATION DATA:
34 APPLICATION NUMBER: US/08/331,397B
35 FILING DATE: 28-OCT-1994
36 CLASSIFICATION: 435
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: US 07/767,331
39 FILING DATE: 30-SEP-1991
40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: US 07/596,289
42 FILING DATE: 12-OCT-1990
43 ATTORNEY/AGENT INFORMATION:
44 NAME: Hunter, Tom
45 REGISTRATION NUMBER: 38,498
46 REFERENCE/DOCKET NUMBER: 015280-126120US
47 TELECOMMUNICATION INFORMATION:
48 TELEPHONE: (415) 543-9600
49 TELEFAX: (415) 543-5043
50 INFORMATION FOR SEQ ID NO: 34:
51 SEQUENCE CHARACTERISTICS:
52 LENGTH: 248 amino acids
53 TYPE: amino acid
54 TOPOLOGY: linear
55 MOLECULE TYPE: protein
56 US-08-331-397B-34

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QY	82	QKHKDAIYTVKSSSTMYMLSLTSEDSAVYYR-----WPEDDMGOGILTVSSEG	135
Db	63	DYVKGFTTISRDNARNTLYLDMSRLKSEDTALITSCARGLWGAMFPAIYKGGILTVSSGC	122
QY	136	KSSGSGSESEKPG-DVVMTPNPLSLPVSIGDOASISGRSSGSLHSNGITLYLHWYLQKRPQ	194
Db	123	GSAGSGSGSGGGSDVLMGLSPSLPYSLGQASISGRSSGILVHSNGNTLEWYLQKRGQ	182
QY	195	SPPLLIIYKXSNRFGVPPRFGSGSGGTDFTLKISRVAEDDLGYVFCSSOSTHVPYTFGGGT	252
Db	183	SPPLLIIYKXSNRFGVPPRFGSGSGGTDFTLKISRVAEDDLGYVFCSSSHVPTFFSGT	242
QY	255	KLEIK 259	
Db	243	KLEIK 247	

US-08-759-804A-34

Result 11

Sequence 34 Application US/08759804A

Patent No. 5990296

GENERAL INFORMATION:

APPLICANT: Pastan, Ira

APPLICANT: Millingham, Mark

APPLICANT: Fitzgerald, David J.

APPLICANT: Brinkmann, Ulrich

APPLICANT: Pal, Lee

TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/759,804A

FILING DATE: 03-DEC-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/331,398

FILING DATE: 28-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/767,331

FILING DATE: 30-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/596,289

FILING DATE: 12-OCT-1990

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen L.

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 016580-126140US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 248 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-759-804A-34

Best Local Similarity 63.7%; Pred. No. 1.5e-68;
Matches 156; Conservative 29; Mismatches 53; Indels 7; Gaps 2;

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QY 22 VQLQOOSGAELVRPGASVTLSCKASGYTFDYEIHVWQTPVHGLEWIGAIDPETGTAYN 81
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 VKLVESGGGLVQGGSGIKLSKATSGFTFSDYMYWVRQPEKRELEWAVASINDSSAAYS 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 82 QKFKDKAIVTVDKSSSTAYMELSLTSEDAVYYTR-----WFDWQGLTVYSAAG 135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 DTVVGRFTTISRDNAKRNLLYLQMSRLEKSEDAITSCARGLAMGAFWYWGQGLTVYSSGG 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 136 KSSGSGSESRKPG-DVYVTPNPILPVSIGDQASISCRSSQSLHNSGITYLHMYLQKPGQ 194
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 GSGSGGGSGGGGSDVMTQSPSLPVSIGDQASISCRSSQSLHNSGITYLHMYLQKPGQ 182
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 195 SPKLLIKVSNRFGVDRFRSGSGGDTFLTKISRVAEADLVGYFCOSGTHVPYFGGCT 254
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 183 SPKLLIKVSNRFGVDRFRSGSGGDTFLTKISRVAEADLVGYFCOSGTHVPYFGGCT 242
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 255 KLEIK 259
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 243 KLEIK 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 12
US-09-070-637-20
; Sequence 20; Application US/09070637A
; Patent No. 6133722
; GENERAL INFORMATION:
; APPLICANT: SIMERS, NATHAN O.
; APPLICANT: YARNOLD, SUSAN
; APPLICANT: SENTER, PETER D.
; TITLE OF INVENTION: RECOMBINANT ANTIBODY-ENZYM FUSION PROTEINS
; FILE REFERENCE: 9197F-83-1
; CURRENT APPLICATION NUMBER: US/09/070,637A
; EARLIER APPLICATION NUMBER: 60/045,888
; EARLIER FILING DATE: 1997-05-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 20
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence for L49-sfv-bl including Pels leader
US-09-070-637-20

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Query Match 56.7%; Score 788.5; DB 4; Length 638;
Best Local Similarity 60.4%; Pred. No. 2.7e-66;
Matches 165; Conservative 31; Mismatches 60; Indels 17; Gaps 5;

```

QY 10 LLAASAASAPAAVQLOOSGAELVRPGASVTLSCKASGYTFDYEIHVWQTPVHGLEWIG 69
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 12 LLLLAAPAAAEVLOQSGPSLVKPSOTLSLTSVIGDSTSGYMWIKPFGNKLEIYWG 71
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 70 AIDPETGTAYNOKFKDKAIVTVDKSSSTAYMELSLTSEDAVY-----YTRWF 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 72 YIS-DSGITYYNPISLKSRISITRDTSKNYLLQNLNFYADATATYCARPLATAYYA-M 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 EDWQGLTVYSAEGKSS-----GSGSRSKPGDVYVMTNPISLTVSLGDDASISCRASQSL 176
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 129 DYWGQGLTVYVSGSGSGSKPGSGEGSTAGDFVMTQTPISLTVSLGDDASISCRASQSL 188
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 177 LHSNGITYLHMYLQKPGQSPKLLIKVSNRFGVDRFRSGSGGDTFLTKISRVAEADLVG 236
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 189 VHSNGNTLHMYLQKPGQSPKLLIKVSNRFGVDRFRSGSGGDTFLTKISRVAEADLVG 248
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 237 VYFCSQSTHVPYTFGGGTKLEIKEKLISEDL 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 249 VYFCSQSTHVPYTFGGGTKLEIKRTP-VSEKQL 280
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 13
US-08-403-853-18
; Sequence 18; Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:

```

; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORRT, Alex A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALBY, Robyn L.
; APPLICANT: POWER, Barbara E.
; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; City: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,853
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU93/00491
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 4973
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/189/CHAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-403-853-18

```

Query Match 55.1%; Score 767; DB 2; Length 273;
Best Local Similarity 59.5%; Pred. No. 9.1e-65;
Matches 156; Conservative 28; Mismatches 64; Indels 14; Gaps 3;

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QY 10 LLAASAASAPAAVQLOOSGAELVRPGASVTLSCKASGYTFDYEIHVWQTPVHGLEWIG 69
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 12 LLLLAAPAAAOVLOOOSGAELVKGASVMSKASGTYFTTNMHWKQSGQGLEWIG 71
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 70 AIDPETGTAYNOKFKDKAIVTVDKSSSTAYMELSLTSEDAVY-----YTRWF 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 72 IFYNGNDTGYNOKFKDKAIVTVDKSSSTAYMELSLTSEDAVYCARSGSYRDGDF 131
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 EDWQGLTVYSAEGKSSGSGSKPGDVYVMTNPISLTVSLGDDASISCRASQSLHNSN 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 132 DYWGQGLTVYVSGGGGSGSGGSDIELTQTSSLSASLGDRTYISCRASQDI--SN 189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GITYLHMYLQKPGQSPKLLIKVSNRFGVDRFRSGSGGDTFLTKISRVAEADLVGYFC 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 190 ---LYNMVQNPSTVTKLLIYYTSNLSHSEVPSSFGSGSGTDTXSLTISNLEQEDTATYRC 246
QY 241 SQSHVPTPTGGGTKEIKEEK 262
Db 247 QODETLPFTFGGTKEIRDYK 268

RESULT 14

US-08-875-811-53
Sequence 53, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-53

Query Match 54.8%; Score 762; DB 3; Length 365;
Best Local Similarity 59.9%; Pred. No. 4e-64;

Matches 145; Conservative 43; Mismatches 50; Indels 4; Gaps 2;

QY 22 VOLOQSGAEIVRGASVYLSCKASGYTFDTYELHWVROTTPVHGLEWIGAIDPETGCTAYN 81
Db 120 VKLOQSGPELKKPGETVYKISCKASGYTFDTYGNMVKQAPGKGLKMGMINITYGESIYA 179
QY 82 QKFRDKAIVTVDKSSSTAYMELSLTSEDSAYYYTRWF--EDWGQGLTVTVSAEGKSS 138
Db 180 DDFGRFAFLETSAASAAYLQINNLEKNEEDATYFCARFAIKGDYWGQGTTVTVSSGGGGS 239
QY 139 GSGSESKPG--DYVMTNPPLSLPVSLGDOASISCRSSQSLHNSNGITYLHWYLOKPGOSPK 197
Db 240 GGGGSGGGSDIYLTQSPFSPNPTLTGTSASISCRSTKSLHNSNGITYLHWYLOKPGOSPO 299

QY 198 LLIYKVNRRSGVDPDRFSGSGSTDTFLKISRVEADLGVTCSSSTAVPTFGGCTKLE 257
Db 300 LLIIQMSNLSASGVDRSSSGTDTFLRISREAEADVGVYCAONLEIPTFGGTLE 359
QY 258 IK 259
Db 360 IK 361

RESULT 15

US-08-875-811-55
Sequence 55, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-55

Query Match 54.8%; Score 762; DB 3; Length 366;
Best Local Similarity 59.9%; Pred. No. 4e-64;

Matches 145; Conservative 43; Mismatches 50; Indels 4; Gaps 2;

QY 22 VOLOQSGAEIVRGASVYLSCKASGYTFDTYELHWVROTTPVHGLEWIGAIDPETGCTAYN 81
Db 3 VKLOQSGPELKKPGETVYKISCKASGYTFDTYGNMVKQAPGKGLKMGMINITYGESIYA 62
QY 82 QKFRDKAIVTVDKSSSTAYMELSLTSEDSAYYYTRWF--EDWGQGLTVTVSAEGKSS 138
Db 63 DDFGRFAFLETSAASAAYLQINNLEKNEEDATYFCARFAIKGDYWGQGTTVTVSSGGGGS 122
QY 139 GSGSESKPG--DYVMTNPPLSLPVSLGDOASISCRSSQSLHNSNGITYLHWYLOKPGOSPK 197
Db 123 GGGGSGGGSDIYLTQSPFSPNPTLTGTSASISCRSTKSLHNSNGITYLHWYLOKPGOSPO 182

OY 198 LLITKVSNRSGVPPDRSGSGSGTDTFTLKISRVEAEDDGVYFCSQSTHWPTFGGKLE 257
Db 193 LLITQMSNLAGVPPDRSGSGSGTDTFTLRISRVEAEDVGYCAONLEIPRTFGGKLE 242
OY 258 IK 259
Db 243 IK 244

Search completed: January 18, 2002, 01:24:42
Job time: 2604 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2002, 00:43:38 ; Search time 37.19 Seconds

(without alignments)
550,980 Million cell updates/sec

Title: US-09-358-321c-32

Perfect score: 1391
Sequence: 1 MVSALVLYVLAARAAHSAFA.....FGGKTKEKEKLEEDL 269

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-68:*
1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	748.5	53.8	249	2 S41374	single chain Fv an
2	662.5	47.6	268	2 A56446	Ig heavy chain V r
3	636.5	45.8	233	2 JCS5322	p53 specific singl
4	563	40.5	112	2 E27887	Ig kappa chain V r
5	562	40.4	112	2 S32189	Ig kappa chain V r
6	558	40.1	118	2 PT0359	Ig kappa chain V r
7	558	40.1	131	2 B34904	Ig kappa chain pre
8	554	39.8	112	2 D27887	Ig kappa chain V r
9	554	39.8	112	2 S53750	antibody Fab Jel 1
10	554	39.8	115	2 S60066	Ig kappa chain V r
11	554	39.8	131	2 B32513	Ig kappa chain pre
12	554	39.8	131	2 C34904	Ig kappa chain pre
13	552	39.7	111	2 PLO257	Ig kappa chain V r
14	552	39.7	112	2 A27887	Ig kappa chain V r
15	551	39.6	115	2 S38715	Ig kappa chain V r
16	551	39.6	131	2 B30577	Ig kappa chain pre
17	549	39.5	112	2 B27887	Ig kappa chain pre
18	547	39.3	112	2 B31485	Ig kappa chain V r
19	547	39.3	113	2 B41940	Ig kappa chain V r
20	546	39.3	112	2 C27887	Ig kappa chain V r
21	544	39.1	131	2 G34903	Ig kappa chain pre
22	542	39.0	131	2 D34904	Ig kappa chain pre
23	541	38.9	112	2 A49715	Ig kappa chain V r
24	538	38.7	131	2 PT0178	Ig kappa chain pre
25	537	38.6	131	2 D29380	Ig kappa chain pre
26	534	38.4	113	1 KVM526	Ig kappa chain V r
27	534	38.4	113	2 PLO205	anti-DNA autoantib
28	534	38.4	132	2 PH0106	anti-digoxin trans
29	534	38.4	219	2 S16112	Ig kappa chain V r

30	531	38.2	131	2 S52449	Ig kappa chain V r
31	529	38.0	112	2 A31807	Ig kappa chain V r
32	527	37.9	131	2 B39276	Ig kappa chain pre
33	526	37.8	107	2 D32530	Ig kappa chain V r
34	524	37.7	110	2 S26335	Ig kappa chain V r
35	523	37.6	113	2 PLO203	Ig kappa chain V r
36	522	37.5	217	2 S42772	anti-DNA autoantib
37	522	37.5	219	2 S52028	Ig kappa chain - m
38	521	37.5	219	2 PC4203	Ig kappa chain (mo
39	520	37.4	219	2 S38865	Ig kappa chain - m
40	519.5	37.3	130	2 C29380	Ig kappa chain pre
41	519	37.3	112	2 E27887	Ig kappa chain V r
42	513	36.9	112	2 S38719	Ig kappa chain V r
43	512	36.8	103	2 PH030	Ig light chain V r
44	512	36.8	108	2 E35530	Ig light chain V r
45	510	36.7	114	2 A32967	Ig kappa chain V r

ALIGNMENTS

```

RESULT 1
S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Artsenko, O.; Weiler, E.W.; Nuentz, K.; Conrad, U.
Submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv ant
A:Reference number: S41374
A:Accession: S41374
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL:229480

Query Match          53.8%: Score 748.5; DB 2; Length 249;
Best Local Similarity 61.1%: Pred. No. 1.4e+48;
Matches 151; Conservative 29; Mismatches 56; Indels 11; Gaps 3;

QY 22 VOLQSGAELVREPASVLTSCRASGYTFDYELHMYRQTPVHGLEMGALDPEFGTRAYN 81
    |||||
Db 2 VOLQSGAELVREPASVLTSCRASGYTFDYELHMYRQTPVHGLEMGALDPEFGTRAYN 61

QY 82 QKFDKRLIVVDKSSRAYWELSLTSEDASVAYYTRMFED-----WGQGLVTVSA 133
    |||||
Db 62 PRFDKRLITADTSSNAYLLSLTSEDVAYYCAR--RDTLYTSLGTYWGQSTVIVS 119

QY 134 EGKSSGSGSESRPG-DVWMTPNPLSLVSLGDOASISCRSSQSLHNSGITVLYHMYLOKP 192
    |||||
Db 120 RGGSSGSGSGSGSDIELHQSPSPVYIPGESVTSICSSKSLXYSDDSYLFMFLQRP 179

QY 193 GQSPKLLIKYVSNRFSVPDPRESGSGGDTFLIKIRVAVEDLVGYFGQSTHYVTGG 252
    |||||
Db 180 GQSPKLLIKYVSNRFSVPDPRESGSGGDTFLIKIRVAVEDLVGYFGQSTHYVTGG 239

QY 253 GTRKLEIK 259
    |||||
Db 240 GTRKLEIK 246

RESULT 2
A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C:Species: Mus musculus (house mouse)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C:Accession: A56446
R:Tang, P.M.; Folitz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally ic
A:Reference number: A56446; M13:95229583

```

A: Title: A novel class of anti-DNA antibodies identified in BALB/c mice.
R: Shennar, R.; Kleiner, G.; Turken, A.; Papazian, L.; Diamond, B.
J. Exp. Med. 173, 287-296, 1991

```

A:Reference number: PT0352; MUID:91108325
A:Accession: PT0359
A:Molecule type: mRNA
A:Residues: 1-118 <SH2>
A:Experimental source: strain BALB/c
C:Comment: This protein is an anti-double-stranded DNA antibody.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:19-98/Domain: immunoglobulin homology <IMM>

Query Match          40.1%, Score 558; DB 2; Length 118;
Best Local Similarity 95.5%; Pred. No. 8e-35;
Matches 107; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 148 DVMVTPNPPLSLPVSLGGDASISCRSSQSLHNSGTYLHWYLOKPGSPKLLIYKVSNR 207
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4 DVMVMTQPLSLPLVSLGGDASISCRSSQSLVHNSGTYLHWYLOKPGSPKLLIYKVSNR 63
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 208 SGVPDRFSGSGGTDFTLTKISRVEADLGIVYFCSGSTHVPYTFGGGTLEIK 259
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 64 SGVPDRFSGSGGTDFTLTKISRVEADLGIVYFCSGSTHVPYTFGGGTLEIK 115
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
B34904
1g kappa chain precursor V region (12-40 and 5-14) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C:Accession: B34904; H34903
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-re-
A:Reference number: A34903; MUID:90094387
A:Accession: B34904
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <BRD>
A:Cross-references: GB:M32384; GB:J05237; GB:J05238; NID:963656; PIDN:AAA61589.1; PID:g
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match          40.1%, Score 558; DB 2; Length 131;
Best Local Similarity 95.5%; Pred. No. 9.1e-35;
Matches 107; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 148 DVMVTPNPPLSLPVSLGGDASISCRSSQSLHNSGTYLHWYLOKPGSPKLLIYKVSNR 207
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 20 DVMVMTQPLSLPLVSLGGDASISCRSSQSLVHNSGTYLHWYLOKPGSPKLLIYKVSNR 79
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 208 SGVPDRFSGSGGTDFTLTKISRVEADLGIVYFCSGSTHVPYTFGGGTLEIK 259
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 80 SGVPDRFSGSGGTDFTLTKISRVEADLGIVYFCSGSTHVPYTFGGGTLEIK 131
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
D27887
1g kappa chain V region (H36-2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C:Accession: D27887
R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a c
A:Reference number: A31043; MUID:86300658
A:Accession: D27887
A:Molecule type: DNA
A:Residues: 1-112 <CAR>
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus
C:Superfamily: immunoglobulin V region; immunoglobulin homology

```

```

C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match          39.8%; Score 554; DB 2; Length 112;
Best Local Similarity 94.6%; Pred. No. 1,5e-34;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVMVTPNPLSLPVSLGQASISCRSSQSLHSGNGITYLHWYLOKPGQSKRLLYKYSNRF 207
      |||||
Db 1 DVMVTQPLSLPVSLGQASISCRSSQSLHSGNGNTYLLHWYLOKPGQSKRLLYKYSNRF 60

QY 208 SGVDFRRSGSSGTFPLKISRVEADLGYFCSQSTHVPYTFGGGTKLEIK 259
      |||||
Db 61 SGVDFRRSGSSGTFPLKISRVEADLGYFCSQSTHVPYTFGGGTKLEIK 112

RESULT 9
553750
antibody Fab Jcl 103 light chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C:Accession: S53750
R:POKulnir, F.R.; Bouthillier, F.; Li, Y.; Kuderova, A.; Lee, J.; Cygler, M.
J. Mol. Biol. 243, 283-297, 1994
A:Title: Preparation, characterization and crystallization of an antibody Fab
A:Reference number: S53750; MUID:95018269
A:Accession: S53750
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <POK>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match          39.8%; Score 554; DB 2; Length 112;
Best Local Similarity 95.5%; Pred. No. 1,5e-34;
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVMVTPNPLSLPVSLGQASISCRSSQSLHSGNGITYLHWYLOKPGQSKRLLYKYSNRF 207
      |||||
Db 1 DVMVTQPLSLPVSLGQASISCRSSQSLHSGNGNTYLLHWYLOKPGQSKRLLYKYSNRF 60

QY 208 SGVDFRRSGSSGTFPLKISRVEADLGYFCSQSTHVPYTFGGGTKLEIK 259
      |||||
Db 61 SGVDFRRSGSSGTFPLKISRVEADLGYFCSQSTHVPYTFGGGTKLEIK 112

RESULT 10
560066
Ig kappa chain V region (monoclonal antibody C3) [validated] - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Feb-1996 #sequence_revision 10-Oct-1997 #text_change 23-Mar-2001
C:Accession: S60066
R:Wien, M.W.; Fillman, D.J.; Stura, E.A.; Guillot, S.; Delpeyroux, F.; Crainic, R.;
Nat. Struct. Biol. 2, 232-243, 1995
A:Title: Structure of the complex between the fab fragment of a neutralizing antioo
A:Reference number: S60066; MUID:95292109
A:Accession: S60066
A:Molecule type: mRNA
A:Residues: 1-115 <WIE>
A:Cross-references: EMBL:X84697; NID:g773226
R:Wien, M.W.; Hogle, J.M.
Submitted to the Brookhaven Protein Data Bank, January 1995
A:Reference number: A52979; PDB:1FPT
C:Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 1-23,'S',25
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status experimental

Query Match          39.8%; Score 554; DB 2; Length 115;

```

Best Local Similarity 95.5%; Pred. No. 1.5e-34;
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVMTPNPISLPVSLGDQASISCRSSQSLHNSGITYLHWYLOKPGSPKLLIKVSNRF 207
|||||
Db 20 DVMTQTPISLPVSLGDQASISCRSSQSLVHNSGNTYLMWYLOKPGSPKLLIKVSNRF 60

QY 208 SGVPDRFSGSGGTDFTLKISRVEADLGIVFCQSSTHVPYTFGGGTLEIK 259
|||||
Db 61 SGVPDRFSGSGGTDFTLKISRVEADLGIVFCQSSTHVPYTFGGGTLEIK 112

RESULT 11

B32513
Ig kappa chain precursor V region (MRL4) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C/Accession: B32513
R/Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A/Title: Immunoglobulin kappa light chain variable region gene complex organization and
A/Reference number: A94689; MUID:88331394
A/Accession: B32513
A/Molecule type: DNA
A/Residues: 1-131 <KOF>
A/Cross-references: GB:M20826; NID:9196937; PID:AAA38843.1; PID:9196938
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 554; DB 2; Length 131;
Best Local Similarity 95.5%; Pred. No. 1.8e-34;
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVMTPNPISLPVSLGDQASISCRSSQSLHNSGITYLHWYLOKPGSPKLLIKVSNRF 207
|||||
Db 20 DVMTQTPISLPVSLGDQASISCRSSQSLVHNSGNTYLMWYLOKPGSPKLLIKVSNRF 79

QY 208 SGVPDRFSGSGGTDFTLKISRVEADLGIVFCQSSTHVPYTFGGGTLEIK 259
|||||
Db 80 SGVPDRFSGSGGTDFTLKISRVEADLGIVFCQSSTHVPYTFGGGTLEIK 131

RESULT 12

C34904
Ig kappa chain precursor V region (3-24) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
C/Accession: C34904; J31485
R/Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A/Title: Active site structure and antigen binding properties of idiotypically cross-react
A/Reference number: A34903; MUID:90094387
A/Accession: C34904
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-131 <BED>
R/Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J. Biol. Chem. 264, 1565-1569, 1989
A/Title: Comparison of variable region primary structures within an anti-fluorescein idi
A/Reference number: A31485; MUID:89109167
A/Accession: J31485
A/Status: preliminary
A/Molecule type: Protein
A/Residues: 20-52 <BE2>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 554; DB 2; Length 131;
Best Local Similarity 94.6%; Pred. No. 1.8e-34;

Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVMTPNPISLPVSLGDQASISCRSSQSLHNSGITYLHWYLOKPGSPKLLIKVSNRF 207
|||||
Db 20 DVMTQTPISLPVSLGDQASISCRSSQSLVHNSGNTYLMWYLOKPGSPKLLIKVSNRF 79

QY 208 SGVPDRFSGSGGTDFTLKISRVEADLGIVFCQSSTHVPYTFGGGTLEIK 259
|||||
Db 80 SGVPDRFSGSGGTDFTLKISRVEADLGIVFCQSSTHVPYTFGGGTLEIK 131

RESULT 13

P10257
Ig kappa chain V region (anti-DNA, DP1VK) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C/Accession: P10257
R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and soma
A/Reference number: P10231; MUID:90111618
A/Accession: P10257
A/Molecule type: mRNA
A/Residues: 1-111 <SHU>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-95/Domain: immunoglobulin homology <IMM>
F:24-39/Region: complementarity-determining 1
F:40-54/Region: framework 2
F:55-61/Region: complementarity-determining 2
F:62-93/Region: framework 3
F:94-102/Region: complementarity-determining 3
F:103-111/Region: framework 4

Query Match 39.7%; Score 552; DB 2; Length 111;
Best Local Similarity 95.5%; Pred. No. 2.1e-34;
Matches 106; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVMTPNPISLPVSLGDQASISCRSSQSLHNSGITYLHWYLOKPGSPKLLIKVSNRF 207
|||||
Db 1 DVMTQTPISLPVSLGDQASISCRSSQSLVHNSGNTYLMWYLOKPGSPKLLIKVSNRF 60

QY 208 SGVPDRFSGSGGTDFTLKISRVEADLGIVFCQSSTHVPYTFGGGTLEIK 258
|||||
Db 61 SGVPDRFSGSGGTDFTLKISRVEADLGIVFCQSSTHVPYTFGGGTLEIK 111

RESULT 14

A27887
Ig kappa chain V region (H37-60) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C/Accession: A27887
R/Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A/Title: Structural and functional implications of a restricted antibody response to
A/Reference number: A91043; MUID:86300658
A/Accession: A27887
A/Molecule type: DNA
A/Residues: 1-112 <CAT>
A/Experimental source: strain Balb/c
A/Note: this sequence was determined from the germ-line gene
C/Comment: This chain was isolated from a hybridoma protein that binds influenza vi
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 39.7%; Score 552; DB 2; Length 112;
Best Local Similarity 93.8%; Pred. No. 2.1e-34;
Matches 105; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 18, 2002, 01:24:48 ; Search time 26.45 Seconds
(without alignments)
372.886 Million cell updates/sec

Title: US-09-358-321c-32

Perfect score: 1391
Sequence: 1 WSAIVLVYLLAAAHSAFA.....FGGCTKLEKEKLESEEDL 269

Scoring table: BLOSUM62
Gapcp 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	534	38.4	113	1	KV2F_MOUSE
2	460	33.1	113	1	KV2F_HUMAN
3	457	32.9	113	1	KV2D_HUMAN
4	454	32.6	113	1	KV2E_MOUSE
5	454	32.6	117	1	KV2E_HUMAN
6	445.5	32.0	119	1	HV07_MOUSE
7	436	31.3	112	1	KV2D_MOUSE
8	435	31.3	113	1	KV2B_HUMAN
9	431.5	31.0	115	1	KV2A_HUMAN
10	431.5	31.0	137	1	HV11_MOUSE
11	423	30.4	138	1	HV48_MOUSE
12	420	30.2	113	1	KV2F_MOUSE
13	417.5	30.0	112	1	KV2C_HUMAN
14	411	29.5	117	1	HV12_MOUSE
15	411	29.5	117	1	HV13_MOUSE
16	409	29.4	117	1	HV49_MOUSE
17	407.5	29.3	118	1	HV51_MOUSE
18	405.5	29.2	120	1	HV50_MOUSE
19	405	29.1	117	1	HV09_MOUSE
20	403	29.0	120	1	HV03_MOUSE
21	400	28.8	140	1	HV02_MOUSE
22	393	28.3	136	1	HV15_MOUSE
23	392	28.2	117	1	HV10_MOUSE
24	391	28.1	117	1	HV04_MOUSE
25	388	27.9	113	1	KV2C_MOUSE
26	383.5	27.6	134	1	KV4C_HUMAN
27	383	27.5	133	1	KV4B_HUMAN
28	382.5	27.5	114	1	KV4A_HUMAN
29	381	27.4	112	1	KV2A_MOUSE
30	381	27.4	117	1	HV05_MOUSE
31	381	27.4	117	1	HV14_MOUSE
32	380	27.3	117	1	HV06_MOUSE
33	376.5	27.1	108	1	KV1_CANFA

34	376.5	27.1	111	1	KV3H_MOUSE	P01660 mus musculu
35	371.5	26.7	111	1	KV3C_MOUSE	P01656 mus musculu
36	371.5	26.7	111	1	KV3L_MOUSE	P01664 mus musculu
37	370.5	26.6	111	1	KV3R_MOUSE	P01670 mus musculu
38	370	26.6	121	1	HV01_MOUSE	P01745 mus musculu
39	368.5	26.5	111	1	KV3A_MOUSE	P01654 mus musculu
40	365.5	26.3	111	1	KV3D_MOUSE	P03977 mus musculu
41	363.5	26.1	111	1	KV3E_MOUSE	P01671 mus musculu
42	363.5	26.1	131	1	KV3I_MOUSE	P01661 mus musculu
43	363	26.1	112	1	KV3B_MOUSE	P01655 mus musculu
44	362.5	26.1	111	1	KV3J_MOUSE	P01662 mus musculu
45	362.5	26.1	111	1	KV3T_MOUSE	P01672 mus musculu

ALIGNMENTS

RESULT	ID	QUERY	STANDARD	PRT	113 AA
AC	P01631	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	IG KAPPA CHAIN V-II REGION 26-10.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE.				
RC	STRAIN-A/J;				
RX	MEDLINE-83178921; Pubmed=6404298;				
RA	Novotny J., Margolies M.N.;				
RT	"Amino acid sequence of the light chain variable region from a mouse				
RT	anti-digoxin hydridoma antibody."				
RL	Biochemistry 22:1153-1158(1983).				
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA				
CC	PROTEIN THAT BINDS DIGOXIN.				
DR	PIR: A01914; KWS26.				
DR	InterPro: IPR003006; Ig_MHC.				
DR	InterPro: IPR003596; Ig_V.				
DR	Pfam: PF00047; Ig, 1.				
DR	SMART: SM00406; IgV, 1.				
KW	Immunoglobulin V region; Monoclonal antibody; Hybridoma.				
FT	DOMAIN 1 23				
FT	DOMAIN 2 39				
FT	DOMAIN 3 54				
FT	DOMAIN 4 61				
FT	DOMAIN 5 93				
FT	DOMAIN 6 102				
FT	DOMAIN 7 112				
FT	DOMAIN 8 123				
FT	DISULFID 93				
FT	NON_TER 113				
SO	SEQUENCE 113 AA; 12273 MW; F9F39CE94984C2A CRC64;				
Query Match	38.4%; Score 534; DB 1; Length 113;				
Best Local Similarity	92.0%; Pred. No. 7.6e-38;				
Matches 103; Conservative	4; Mismatches 5; Indels 0; Gaps 0;				
QY	148 DVVMTFNPFLSPVSLGDAASISCRSSOSLHNSNTLHMYLTKPKPGSPPLTLTKYSNRF 207				
DB	1 DVVMTQTPLSPLVSLGDAASISCRSSOSLHNSNTLHMYLTKPKPGSPPLTLTKYSNRF 60				
QY	208 SGVPRFSGSGSGTDFTKISRVAEADLGYFCSQSTHVPYTFGGGTKLEIK 259				
DB	61 SGVPRFSGSGSGTDFTKISRVAEADLGYFCSQSTHVPYTFGGGTKLEIK 112				
RESULT	2				
KV2F_HUMAN	STANDARD;				
ID	KV2F_HUMAN				
	PRT; 133 AA.				

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AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION RPMI 6410 PRECURSOR.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbe H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT II."
RL Nucleic Acids Res. 13:6499-6513(1985).
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CC -----
DR EMBL; 200020; CAAT7315.1; -.
DR PIR; A01890; K2HURP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 20
FT DOMAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 60 74 FRAMEWORK 2.
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 82 113 FRAMEWORK 3.
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 123 132 FRAMEWORK 4.
FT DISULFID 43 113 BY SIMILARITY.
FT NON TER 133
SQ SEQUENCE 133 AA; 14707 MW; 513C6A3673009EE CRC64;

Query Match 33.1%; Score 460; DB 1; Length 133;
Best Local Similarity 77.9%; Pred. No. 1.3e-31;
Matches 88; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 147 GDVWTPPLPLPSLGDQASISCRSSQSLHNSGITYLHWYQKQSGSKLLIKVSNR 206
DB 20 GDVWTPPLPLPSLGDQASISCRSSQSLVSDGNTYLNWFGQRCGSPRRILIKVSNR 79
QY 207 FSGVDFRSGSGSGTDFTLKISRVEADLVGYFCOSTHVPYFGGKTLEIK 259
DB 80 DSGVDFRSGSGSGTDFTLKISRVEADLVGYFCOSTHVPYFGGKTLEIK 132

RESULT 3
KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION TEM.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEM).

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RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
RT primary amyloidosis."
RL Biochemistry 12:3763-3780(1973).
RN [2]
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEM).
RX MEDLINE=73166638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
RT patient with plasma cell dyscrasia and amyloidosis."
RL J. Clin. Invest. 52:1276-1281(1973).
CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSPLASIA AND AMYLOIDOSIS.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
DR PIR; A01888; K2HUTW.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
FT DOMAIN 1 23
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 40 54 FRAMEWORK 2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 62 93 FRAMEWORK 3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 103 112 FRAMEWORK 4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON TER 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C8F81E1843CA CRC64;

Query Match 32.9%; Score 457; DB 1; Length 113;
Best Local Similarity 76.8%; Pred. No. 1.9e-31;
Matches 86; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 148 DVWTPPLPLPSLGDQASISCRSSQSLHNSGITYLHWYQKQSGSKLLIKVSNR 207
DB 1 DVWTPPLPLPSLGDQASISCRSSQSLHNSGITYLHWYQKQSGSKLLIKVSNR 60
QY 208 SGVDFRSGSGSGTDFTLKISRVEADLVGYFCOSTHVPYFGGKTLEIK 259
DB 61 SGVDFRSGSGSGTDFTLKISRVEADLVGYFCOSTHVPYFGGKTLEIK 112

RESULT 4
KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION 17S29.1.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Hybridoma;
RX MEDLINE=85128968; PubMed=6441768;
RA Aebersold R., Herbst H., Grutler T., Chang J.Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide."
RL Hoppe-Seivler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -1- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
DR PIR; A01912; KVM517.

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DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 KM Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 40 54 FRAMEWORK 2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 62 93 FRAMEWORK 3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 103 112 FRAMEWORK 4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 32.6%; Score 454; DB 1; Length 113;
 Best Local Similarity 75.9%; Pred. No. 3.4e-31;
 Matches 85; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 148 DVTMPNPPLSLPVSLDDASISCRSSOSLSHNGITLYLHWYLOKPGSPKLIYKVSNR 207
 DB 1 DIVMTQAFNSPVLGTSTASISCRSSKSLSHNGITLYLHWYLOKPGSPQLLYQMSNLA 60

QY 208 SGVPRFRSGSGSGTDFTLKISRVEADLVGYFCQSSTHVPYTFGGGKLEIK 259
 DB 61 ASGVPRFRSGSGSGTDFTLKISRVEADLVGYVYCAHNELEPYTFGGGKLEIK 112

RESULT 5
 ID KV2E_HUMAN STANDARD; PRT; 117 AA.
 AC P06309;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1998 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION GM607 PRECURSOR (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84191506; PubMed=6325927;
 RA Klobbeck H.G., Solomon A., Zachau H.G.;
 RT "Contribution of human V kappa II germ-line genes to light-chain
 RT diversity";
 RL Nature 309:73-76(1984).
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 CC EMBL: J00009; -; NOT_ANNOTATED_CDS.
 DR PIR: A01889; K2HUCM.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 1
 FT CHAIN <1 4
 FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
 FT DOMAIN 5 27 FRAMEWORK 1.
 FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 44 58 FRAMEWORK 2.
 FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 66 97 FRAMEWORK 3.

FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 107 116 FRAMEWORK 4.
 FT DISULFID 27 97 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E559B1 CRC64;

Query Match 32.6%; Score 454; DB 1; Length 117;
 Best Local Similarity 77.9%; Pred. No. 3.5e-31;
 Matches 88; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 147 GDVMTNPPLSLPVSLDDASISCRSSOSLSHNGITLYLHWYLOKPGSPKLIYKVSNR 206
 DB 4 GDVMTQSPPLSLPVTPGEPASISCRSSOSLSHNGITLYLHWYLOKPGSPQLLYIGSNR 63

QY 207 FSGVPRFRSGSGSGTDFTLKISRVEADLVGYFCQSSTHVPYTFGGGKLEIK 259
 DB 64 ASGVPRFRSGSGSGTDFTLKISRVEADLVGYVYCAHNELEPYTFGGGKLEIK 116

RESULT 6
 ID HV07_MOUSE STANDARD; PRT; 139 AA.
 AC P01751; P01752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1998 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Botwell A.L.M., Paaskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NpB family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region";
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THE B1-8 WT CHAIN mRNA WAS CLONED FROM A HYBRIDOMA
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 CC (NPB ANTIBODIES).
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: J00529; AAA38170.1; -
 DR PIR: A02034; MHMS18.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 1 139 IG HEAVY CHAIN V REGION B1-8/186-2.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DOMAIN 118 124 D SEGMENT.
 FT DOMAIN 125 139 JH2 SEGMENT.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 139 139
 SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

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Query Match          32.0%: Score 445.5; DB 1; Length 139;
Best Local Similarity 65.2%: Pred No. 2.2e-30;
Matches 90; Conservative 14; Mismatches 25; Indels 9; Gaps 2;

QY 3 SAIVLYLLAAAHSAFAAYOLOQSGAEIVRPGASVLTSCKASGYTFDYETIHWRQTPV 62
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 4 SCIMLF--LAATATGVHSVOLOQPGAEIVKPGASVLTSCKASGYTFDSYMWVWKCRPG 61
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 63 HGLWGAIDPEGTGTAVNOKFKRAIVTVDKSSSTAVYMERLSSEDSAAVYYTR--- 118
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 62 RGLWGTGRIDPNSGGTIVNEKFKATLVDPKSTATVWLSLTSEDSAAVYYCARIDY 121
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 119 ---WPEDMGGGLVTVSA 133
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 122 GSSYFDYWGQGLTLTVSS 139
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 7
KV2D_MOUSE STANDARD; PRT; 112 AA.
AC P01629;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION 251.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=63055101; PubMed=7141411;
RA Herbst H., Chang J.Y., Abersold R., Braun D.G.;
RT "Murine VK25 isotype sequence: monoclonal antibody 251.3 specific for
RT the group A streptococcal polysaccharide."
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR: A01911; KVMSS1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR KIM Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 24 39 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 40 54 FRAMEWORK 2.
FT DOMAIN 4 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 62 93 FRAMEWORK 3.
FT DOMAIN 6 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 7 103 112 FRAMEWORK 4.
FT DISULFID 123 93 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12221 MW; BD5EF56BD79FBEBC CRC64;

Query Match          31.3%: Score 436; DB 1; Length 112;
Best Local Similarity 74.1%: Pred. No. 1.1e-29;
Matches 83; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGQASISCRSSQSLHNSGITVLYLHWYLOKPGOSPFLLYKYSNRF 207
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 1 DIVMTQAAFSNPNVLTGSTASFSRSLQSGKITVLYLWYLOKPGOSPFLLYKYSNRLA 60
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 208 SGVPRFSGSGSGTDFLTAKISRYEADLGVYFCQSSTHVPYTFGGGTKEIK 259
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 61 SGVPRFSGSGSGTDFLTAKISRYEADLGVYFCQSSTHVPYTFGGGTKEIK 112
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 8
KV2B_HUMAN STANDARD; PRT; 113 AA.
AC P01629;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION 251.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=63055101; PubMed=7141411;
RA Herbst H., Chang J.Y., Abersold R., Braun D.G.;
RT "Murine VK25 isotype sequence: monoclonal antibody 251.3 specific for
RT the group A streptococcal polysaccharide."
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR: A01911; KVMSS1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR KIM Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 24 39 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 40 54 FRAMEWORK 2.
FT DOMAIN 4 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 62 93 FRAMEWORK 3.
FT DOMAIN 6 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 123 93 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12221 MW; BD5EF56BD79FBEBC CRC64;

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AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76253627; PubMed=821524;
RA Riesen W.F., Jaton J.-C.;
RT "Variable region sequence of the light chain from a Waldenström's IgM
RT with specificity for phosphorylcholine."
RL Biochemistry 15:3829-3833(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
DR PIR: A01886; K2HDFR.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR KIM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 24 39 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 40 54 FRAMEWORK 2.
FT DOMAIN 4 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 62 93 FRAMEWORK 3.
FT DOMAIN 6 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 123 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match          31.3%: Score 435; DB 1; Length 113;
Best Local Similarity 74.1%: Pred. No. 1.3e-29;
Matches 83; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGQASISCRSSQSLHNSGITVLYLHWYLOKPGOSPFLLYKYSNRF 207
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 1 DIVMTQAAFSNPNVLTGSTASFSRSLQSGKITVLYLWYLOKPGOSPFLLYKYSSTRD 60
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 208 SGVPRFSGSGSGTDFLTAKISRYEADLGVYFCQSSTHVPYTFGGGTKEIK 259
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 61 SGVPRFSGSGSGTDFLTAKISRYEADLGVYFCQSSTHVPYTFGGGTKEIK 112
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 9
KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION CDM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type)."
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50: 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation."

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Db      62  OGLEWIGELINPNDGRSNVNEKFRKATLVKSSSTAYMQLSLPFEFAVYCARSDGY 121
      117  TRFEDMGOGTLTVSA 133
      122  YCMFYWGGGTITVFS 138

RESULT 12
KVZF_MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION 7534.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody, containing an additional cysteine residue
RT for the isolation of peptides."
RL Biochem. J. 211:173-180(1983).
CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR: A01913; KMS7S.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 39 FRAMEWORK 2.
FT DOMAIN 40 54 FRAMEWORK 3.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 94 102 FRAMEWORK 3.
FT DOMAIN 103 112 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 123 93 FRAMEWORK 4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 30.2%; Score 420; DB 1; Length 113;
Best Local Similarity 71.4%; Pred. No. 2.3e-28;
Matches 80; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 148 DVMATPNPLSLPVSLGDSISCRSSOSLSHNSGITYLHWYLOKPGOSPKLLIKVSNRF 207
      1 DIVVTQTPALVTPGSAVTSICRSSKSLSHNSGNTLYLWFOQRQCCQLTIKWSNLA 60

Db      208  SGVPDRFSGSGSGTDFTLKISRVEADLGVYFCSGSTHVPYTFGGGKLEIK 259
      61  SGVPDRFSGSGSGTAFLLRISRVEADLVGYCMQREVPYTFGGGKLEIK 112

RESULT 13
KVZC_HUMAN STANDARD; PRT; 112 AA.
AC P01616;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION MTL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis."
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01887; K2HUML.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 30.0%; Score 417.5; DB 1; Length 112;
Best Local Similarity 68.8%; Pred. No. 3.6e-28;
Matches 77; Conservative 19; Mismatches 15; Indels 1; Gaps 1;

QY 148 DVMATPNPLSLPVSLGDSISCRSSOSLSHNSGITYLHWYLOKPGOSPKLLIKVSNRF 207
      1 DIVVTQTPALVTPGSAVTSICRSSQDLZSBG-BYLDWLZKRGZEPZLLITLGSNRA 59

Db      208  SGVPDRFSGSGSGTDFTLKISRVEADLGVYFCSGSTHVPYTFGGGKLEIK 259
      60  SGVPDRFSGSGSGTDFTLKISRVEADLVGYCMQALQTPLETFGGTIVEIK 111

RESULT 14
KV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sidley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains."
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR: A02039; MMS4E.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
FT NON_TER 117 117

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 18, 2002, 01:23:53 ; Search time 63.13 Seconds
(Without alignments)
623,274 Million cell updates/sec

Title: US-09-358-321C-32

Perfect score: 1391

Sequence: 1 MSAIVLYVLLAAAHSAFA.....FGGTRKLEIKESDL 269

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_17:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.todent:*
13: sp.virus:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	602.5	43.3	298	11 Q9QYF0	Q9QYF0 mus musc
2	530	38.1	238	11 Q9QYF0	Q9QYF0 mus musc
3	527	37.9	104	11 Q9JL82	Q9JL82 mus musc
4	438	31.5	473	11 Q9D814	Q9D814 mus musc
5	437.5	31.5	114	4 Q9UL80	Q9UL80 homo sapien
6	414	29.8	117	4 Q9QXFO	Q9QXFO mus musc
7	409.5	29.4	463	11 Q9JL84	Q9JL84 mus musc
8	407	29.3	473	11 Q9JL85	Q9JL85 mus musc
9	405	29.1	117	11 Q9QXES	Q9QXES mus musc
10	397	28.5	117	11 Q9JL86	Q9JL86 mus musc
11	397	28.5	119	5 Q9GY22	Q9GY22 schistosoma
12	386.5	27.8	468	11 Q9JL81	Q9JL81 mus musc
13	379.5	27.3	118	11 Q9JL84	Q9JL84 mus musc
14	376.5	27.1	109	11 Q9JL85	Q9JL85 mus musc
15	371.5	26.7	114	11 Q9JL81	Q9JL81 mus musc
16	366	26.3	119	4 Q9UL94	Q9UL94 homo sapien
17	360.5	25.9	124	4 Q9UL92	Q9UL92 homo sapien
18	351.5	25.3	110	11 Q9JL77	Q9JL77 mus musc
19	349	25.1	109	4 Q9UL78	Q9UL78 homo sapien

20	347	24.9	125	4 Q9UL95	Q9UL95 homo sapien
21	346	24.9	150	4 Q9Y298	Q9Y298 homo sapien
22	343.5	24.7	500	4 Q9BRV0	Q9BRV0 homo sapien
23	341	24.5	484	11 Q9JL86	Q9JL86 mus musc
24	336.5	24.2	103	11 Q9JL80	Q9JL80 mus musc
25	335.5	24.1	107	11 Q9ER29	Q9ER29 mus musc
26	334.5	24.0	99	11 Q9JL74	Q9JL74 mus musc
27	334.5	24.0	110	11 Q9UL83	Q9UL83 mus musc
28	332	23.9	109	11 Q9JL85	Q9JL85 mus musc
29	330	23.7	111	11 Q9D9B8	Q9D9B8 mus musc
30	327.5	23.5	116	4 Q9UL89	Q9UL89 homo sapien
31	326.5	23.5	108	4 Q9UL77	Q9UL77 homo sapien
32	319	22.9	109	4 Q9UL86	Q9UL86 homo sapien
33	316.5	22.8	108	4 Q9UL83	Q9UL83 homo sapien
34	315.5	22.7	108	4 Q9UL70	Q9UL70 homo sapien
35	315	22.6	107	4 Q9UL81	Q9UL81 homo sapien
36	314.5	22.6	108	4 Q9UL79	Q9UL79 homo sapien
37	313	22.5	106	5 Q9UL10	Q9UL10 schistosoma
38	312	22.4	109	4 Q9UL85	Q9UL85 mus musc
39	311.5	22.4	214	11 Q9JL85	Q9JL85 mus musc
40	307.5	22.1	157	4 Q95978	Q95978 homo sapien
41	306.5	22.0	101	11 Q9UL78	Q9UL78 mus musc
42	299.5	21.5	97	11 Q9UL76	Q9UL76 mus musc
43	292	21.0	479	11 Q99M22	Q99M22 mus musc
44	285	20.5	487	11 Q99KA4	Q99KA4 mus musc
45	284.5	20.5	120	4 Q9B0A1	Q9B0A1 homo sapien

ALIGNMENTS

RESULT 1
ID Q9QYF0 PRELIMINARY: PRT: 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CN 8 SCFV.
GN CN 8
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=SPLEEN;
RA Shinohara N., Demura T., Fukuda H.;
RL Submitted (Dec-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=SPLEEN;
RA Shinohara N., Demura T., Fukuda H.;
RL Submitted (Dec-1999) to the EMBL/GenBank/DBJ databases.
RT antibody recognizing a cell polarity using a phage display subtraction method.
RT "Isolation of a novel type of vascular cell wall-specific monoclonal antibody recognizing a cell polarity using a phage display subtraction method."
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
DR EMBL: AB036341; BAA88633.1;
DR HSSP: P01607; IRET.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003586; IG_V.
DR Pfam: PF00047; 19; 2.
DR SMART: SM00406; IG; 2.
SQ SEQUENCE 298 AA: 31867 MW: EDP96B8A17004317 CRC64;

Query Match 43.3%; Score 602.5; DB 11; Length 298;
Best Local Similarity 48.4%; Pred. No. 5.7e+45;
Matches 122; Conservative 39; Mismatches 80; Indels 11; Gaps 4;
QY 14 AAASRAVAVOLQSGAELVPGASVTLSCASGYTFTEIHWKQTFVHGLEWGAIDP 73

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Db 33 AAFPMAQVKTQSGGGGKPGSLKLSAAGSDFFSRVMSVWPAQGLWEIENP 92
Qy 74 ETGGANVQKFKDAIVYVDSSTAMELRSITSEDAVY-----YTFWFDMDGCGTL 128
Db 93 DSSITNTPSLKDKFIIISRDNAKNTLYLQMSKYRSEDTALTYCARASVYGHSAVWGQGT 152
Qy 129 VTVSAEGKSGSGSESKPG-DVWMTPNPLSPVSLGDAQSISCRSSQSLHNSGITYLHW 187
Db 153 VTVSSGGSGSGGGGGSDIELTQSPASIASVGETVITTCRASGN-IHN----YLAW 207
Qy 168 YLQKRGSPKLLIKVNSRFGVPRFSGSGSDTFLTKISRVEAEDLGVFCSQSTHWP 247
Db 208 YQKRGKSPOLLVYNAKTADGVPRFSGSGSTQYSLKINSQPEDFGSYCOHFMTTP 267
Qy 248 YTFGGGTLEIK 259
Db 268 YTFGGGTLEIK 279

RESULT 2
Q99M37 PRELIMINARY; PRT; 238 AA.
AC 099M37;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:59477).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR;
RA Strussberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AA02035.1;
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 38.1%; Score 530; DB 11; Length 238;
Best Local Similarity 90.2%; Pred. No. 9.7e-39;
Matches 101; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 148 DVVMTPNPLSPVSLGDAQSISCRSSQSLHNSGITYLHWLQKRGSPKLLIKVNSR 207
Db 20 DVVMTQTPSLPVSIGDAQSISCRSSQSLHNSGITYLHWLQKRGSPKLLIKVNSR 79
Qy 208 SGVPRFSGSGSDTFLTKISRVEAEDLGVFCSQSTHWPYTFGGGTLEIK 259
Db 80 SGVPRFSGSGSDTFLTKISRVEAEDLGVFCSQSHVPTFGSGTLEIK 131

RESULT 3
Q9UL82 PRELIMINARY; PRT; 104 AA.
AC 09UL82;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RA Maikael S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

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CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF206024; AAF69322.1;
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
FT NON_TER 1
FT TER 104
SQ SEQUENCE 104 AA; 11360 MW; 5DABBBFD5F0AA1AE CRC64;

Query Match 37.9%; Score 527; DB 11; Length 104;
Best Local Similarity 96.2%; Pred. No. 5.9e-39;
Matches 100; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 156 LSLPVSIGDAQSISCRSSQSLHNSGITYLHWLQKRGSPKLLIKVNSRFGVPRDS 215
Db 1 LSLPVSIGDAQSISCRSSQSLHNSGITYLHWLQKRGSPKLLIKVNSRFGVPRDS 60
Qy 216 GSGSGTDFTLTKISRVEAEDLGVFCSQSTHWPYTFGGGTLEIK 259
Db 61 GSGSGTDFTLTKISRVEAEDLGVFCSQSTHWPYTFGGGTLEIK 104

RESULT 4
Q9DBL4 PRELIMINARY; PRT; 473 AA.
AC 09DBL4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 1810060009RIK PROTEIN.
GN 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085650; PubMed=11217851;
RA Kawai J., Shnagawa A., Shibata K., Yoshino M., Itoh Y., Ishii Y.,
RA Arkawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirini L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seye T., Shibata K., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whittaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashida Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 408:685-690(2001).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AK007918; BAB25349.1;
DR MGD; MGI:1924014; 1810060009RIK.
DR InterPro: IPR003599; IG.
DR InterPro: IPR003597; IG_C1.
DR InterPro: IPR003600; IG_Like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.

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DR SMART; SM00407; IG1, 3.
 DR SMART; SM00406; IG1, 1.
 DR SMART; SM00410; IG1like; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 31.5%; Score 438; DB 11; Length 473;
 Best Local Similarity 52.5%; Pred. No. 2.9e-30;
 Matches 95; Conservative 21; Mismatches 45; Indels 20; Gaps 3;

QY 7 LVYLLAAAHSAFAVLOOSGAELVRPGASVTLSCKASGYFTDYELHWRQTPVHGLE 66
 DB 6 VFLEFLSVTAGVHCQYQLKSGHGLKPGASVTKSKASGYFTDYELHWRQTPVHGLE 65
 QY 67 WIGALDPETGTAIVNCRFKDAIVYDKSSSTAYMELRLTSEDSAVYYTR-----WF 120
 DB 66 WICKIGPGSGSYNEKFKGKATLADKSSSTAYMQLSLTSEDSAVYFCARSGYDWMF 125
 QY 121 EDNGCGTLVTVSAEGKSSSS-----GSESKGQDV--MTNPPLSLPVSLGDQA 166
 DB 126 AYWCGGLTVTVSAKTTAPSVPLAPVCGGTGSSVTLGCLVKGYPPEPVLTVNSGSL 185
 QY 167 S 167
 DB 186 S 186

RESULT 5
 Q90L80 PRELIMINARY; PRT; 114 AA.
 ID Q90L80;
 AC Q90L80;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL; AF035034; AAD56270.1; -
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG1, 1.
 FT NON_TER 1
 FT NON_TER 114
 SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 31.5%; Score 437.5; DB 4; Length 114;
 Best Local Similarity 76.1%; Pred. No. 4.7e-31;
 Matches 66; Conservative 13; Mismatches 13; Indels 1; Gaps 1;

QY 148 DVVMTNPPLSLPVSLGDQASISCRSSQSLHNSNGITLHWYLOKPGQSKFLIYVNSRF 207
 DB 1 DVVMTQSPPLSLPVTLKPSAISICRSSQSPYSDNGITLHWYLOKPGQSPRRILYVNSRD 60
 QY 208 SGVDFRSGSGSDPTLKISRYEADLGVYFCQSSTH-VPTFGGGLTLEIK 259
 DB 61 SGVDFRSGSGSDPTLKISRYEADLGVYFCQSSTH-VPTFGGGLTLEIK 113

RESULT 6
 Q90XFO PRELIMINARY; PRT; 117 AA.
 ID Q90XFO;
 AC Q90XFO;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Clemens A., Rademakers A., Specht C., Koelsch E.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL; AJ225171; CAB65236.1; -
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG1, 1.
 FT NON_TER 1
 FT NON_TER 117
 SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47EAC CRC64;

Query Match 29.8%; Score 414; DB 11; Length 117;
 Best Local Similarity 69.8%; Pred. No. 5.7e-29;
 Matches 81; Conservative 13; Mismatches 18; Indels 4; Gaps 1;

QY 22 VOLOQSGALVRPGASVTLSCKASGYFTDYELHWRQTPVHGLEWIGALDPETGTAIVN 81
 DB 2 VOLOQSGPELVVRPGASVTKSKASGYFTDYELHWRQTPVHGLEWIGALDPETGTAIVN 61
 QY 82 QKFKDAIVTVKSSSTAYMELRLTSEDSAVYYTR-----WFDWGGGLTVISA 133
 DB 62 QKFKGATLTVKSSSTAYMQLNSLTSEDSAVYYCAROKDYFVWGGGLTVISA 117

RESULT 7
 Q99LC4 PRELIMINARY; PRT; 463 AA.
 ID Q99LC4;
 AC Q99LC4;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE SIMILAR TO RIKEN CDNA 1610060009 GENE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC003435; AAH03435.1; -
 SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BHC30783 CRC64;

Query Match 29.4%; Score 409.5; DB 11; Length 463;
 Best Local Similarity 50.8%; Pred. No. 8.9e-28;
 Matches 94; Conservative 16; Mismatches 50; Indels 25; Gaps 4;

QY 5 IVLYLL-AAAASAFAAVLOOSGAELVRPGASVTLSCKASGYFTDYELHWRQTPVH 63
 DB 6 IVLYLLSGTAGVHS--QVLOQSGHGLKPGASVTKSKASGYFTGYGVSWKQRTGQ 62
 QY 64 GLEWIGALDPETGTAIVNCRFKDAIVYDKSSSTAYMELRLTSEDSAVYYTR----- 118
 DB 63 GLEWGEIIPGSGNTYSEKFKGKATLTVKSSSTAYMQLNSLTSEDSAVYFCARSSYS 122

QY 119 --WEDMGGTLVTVSABGKSSGSGSEKPGDYYVWT-----PNPLSLPVSL 162
 Db 123 YDLFAWMGGLTVFVSAKTPPPSYPLAPGSAQTNMTGLGCLVXGYPEPVTYWN 182
 QY 163 GDQAS 167
 Db 183 GSLS 187

RESULT 8
 099L25 PRELIMINARY: PRT: 473 AA.
 AC 099L25:
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SIMILAR TO RIKEN CDNA 181006009 GENE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC003888; AA03888.1; -
 SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 29.3%; Score 407; DB 11; Length 473;
 Best Local Similarity 48.1%; Pred. No. 1.5e-27;
 Matches 90; Conservative 24; Mismatches 45; Indels 28; Gaps 4;
 QY 6 YLYVLAHAHFAFAVQIQSGALVPRGASVYLSKASGYTFTDYEIHVROTYPVHGL 65
 Db 8 LFFLSYTVGVH--QVQIQSDAELVPRGASVYLSKASGYTFTDHTIHWKQRPQGL 64
 QY 66 EWGAIIDPETGTAYNOKKCAITVYDKSSSTAYMEKRLTSDSAVYYTR----- 118
 Db 65 EWGVIYPRDGSRTKNEKKGATLTADKSSSTAYMQNLSTSDSAVCFSGSLYYG 124
 QY 119 ---WEDMGGTLVTVSABGKSSGSGSEKPGDYYVWT-----PNPLSLPV 160
 Db 125 YGLYFDYVWGCGTTLTVSAAKTPAPVPLAPVCGDTGSSVTLGCLVXGYPEPVTLTW 184
 QY 161 SUGDAS 167
 Db 185 NSGSLSS 191

RESULT 9
 090XE9 PRELIMINARY: PRT: 117 AA.
 AC 090XE9:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Clemens A., Rademakers A., Specht C., Koelsch E.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: AJ225174; CAB55237.1; -
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.

FT NON_TER 1
 FT NON_TER 117
 SQ SEQUENCE 117 AA; 13000 MW; CDDEZAF84D499734 CRC64;

Query Match 29.1%; Score 405; DB 11; Length 117;
 Best Local Similarity 69.8%; Pred. No. 3.5e-28;
 Matches 81; Conservative 11; Mismatches 20; Indels 4; Gaps 1;
 QY 22 VOLQSGALVPRGASVYLSKASGYTFTDYEIHVROTYPVHGLWIGAIIDPETGTAYN 81
 Db 2 VOLQSGELVPRGASVYLSKASGYTFTDYEIMVQVSGKSLWIGIDINPNNGTSYN 61
 QY 82 QKFKAATVYDKSSSTAYMEKRLTSDSAVYYTR-----WEDMGGTLVTVSA 133
 Db 62 QKFKAATLVYDKSSSTAYMQNLSTSDSAVYVCARDRYAMDYWGQTSYVSS 117

RESULT 10
 092IC6 PRELIMINARY: PRT: 117 AA.
 AC 092IC6:
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ANTI-PORCINE VCAV MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C.
 RA Mueller J.P., Gianconi M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
 RA Watts L.M., Evans M.J.;
 RT "Humanized porcine VCAV-specific monoclonal antibodies with chimeric
 RT IgG2/G4 constant regions block human leukocyte binding to porcine
 RT endothelial cells."
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: D07879; AAD00291.1; -
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 117
 SQ SEQUENCE 117 AA; 13122 MW; 4F5B193AFB7E5B CRC64;

Query Match 28.5%; Score 397; DB 11; Length 117;
 Best Local Similarity 67.2%; Pred. No. 1.8e-27;
 Matches 78; Conservative 9; Mismatches 25; Indels 4; Gaps 1;
 QY 22 VOLQSGALVPRGASVYLSKASGYTFTDYEIHVROTYPVHGLWIGAIIDPETGTAYN 81
 Db 2 VOLQSGPOLVPRGASVYLSKASGYTFTDYEIMVQVSGKSLWIGIDINPNNGTSYN 61
 QY 82 QKFKAATVYDKSSSTAYMEKRLTSDSAVYYTR-----WEDMGGTLVTVSA 133
 Db 62 QRLKDAITLVKSSNTAYMGSGPTSDSAVYCTREVSWMFVWGGLTVTVSA 117
 RESULT 11
 09GYZ2 PRELIMINARY: PRT: 119 AA.
 AC 09GYZ2:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE MONOCLONAL ANTI-ID10TYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
 DE (FRAGMENT).

OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Rhabdiorhorea; Neodermata;
 OC Trematoda; Digenea; Strigeidae; Schistosomatidae; Schistosomatidae;
 OC Schistosoma.
 CX NCBI_TaxID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Song X.T., Feng Z.Q., Guan X.H.;
 RT "Amplification, cloning and sequence analysis of the heavy chain
 RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
 RT Schistosoma japonicum."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: AF282622; AAC01452.1; -
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00409; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 DR SMART: SM00410; Ig_Like; 1.
 FT NON_TER 1
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13567 MW; BA893873FDF5FA6AB CRC64;

Query Match 28.5%; Score 397; DB 5; Length 119;
 Best Local Similarity 65.3%; Pred. No. 1.8e-27;
 Matches: 77; Conservative 14; Mismatches 21; Indels 6; Gaps 1;

OY 22 VOLOSGAEIVRGASVTLSCKASGYFTDYELHWKQRPVHGLEWIGALIDPETGTAYN 81
 DB 2 VOLVESGAEIVRGASVTLSCKASGYFTDYELHWKQRPVHGLEWIGALIDPETGTAYN 61
 OY 82 QKFKDAIVTVDKSSSTAYMELSLTSEDSAVYYTYRMPED-----WGQGLTVTVA 133
 DB 62 QKFKDAIVTVDKSSSTAYMELSLTSEDSAVYYTYRMPED-----WGQGLTVTVA 119

RESULT 12
 O99LJ31 PRELIMINARY; PRT; 468 AA.
 AC O99LJ31.
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC003878; AAH03878.1; -
 SQ SEQUENCE 468 AA; 51661 MW; 9635232B3332ADB CRC64;

Query Match 27.8%; Score 386.5; DB 11; Length 468;
 Best Local Similarity 47.3%; Pred. No. 9.4e-26;
 Matches 86; Conservative 26; Mismatches 49; Indels 21; Gaps 4;
 OY 6 VLYVLAASAFAAVALOOSGAELVPGASVTLSCKASGYFTDYELHWKQRPVHGL 65
 DB 6 VIFLMAVYI-GVNSEVQLQOSGAELVPGASVTLSCAGFNKXKSLMHWQRPREGGI 64
 OY 66 EWIGALIDPETGTAYNOKFKDAIVTVDKSSSTAYMELSLTSEDSAVYY-----YTRM 119
 DB 65 EWIGALIDPETGTAYNOKFKDAIVTVDKSSSTAYMELSLTSEDSAVYYCARNLLYGGY 124

OY 120 FEDMGQGLTVTVAEKRSGS-----GSESRPGDV--MTPNLSLVSLDQ 165
 DB 125 YDWGQGLTVTVAEKRSGS-----GSESRPGDV--MTPNLSLVSLDQ 184
 OY 166 AS 167
 DB 185 SS 186

RESULT 13
 O921C4 PRELIMINARY; PRT; 118 AA.
 AC O921C4.
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=BA16/C;
 RA Mueller J.P., Giannotti M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
 RA Matlis L.M., Evans M.J.;
 RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
 RT 1962/64 constant regions block human leukocyte binding to porcine
 RT endothelial cells."
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: U78801; AAD00293.1; -
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 FT NON_TER 1
 FT NON_TER 118
 SQ SEQUENCE 118 AA; 13036 MW; 90EBC559D31EC4FC CRC64;

Query Match 27.3%; Score 379.5; DB 11; Length 118;
 Best Local Similarity 65.0%; Pred. No. 6.1e-26;
 Matches 76; Conservative 11; Mismatches 25; Indels 5; Gaps 1;

OY 22 VOLOSGAEIVRGASVTLSCKASGYFTDYELHWKQRPVHGLEWIGALIDPETGTAYN 81
 DB 2 VOLOSGAEIVRGASVTLSCKASGYFTDYELHWKQRPVHGLEWIGALIDPETGTAYN 61
 OY 82 QKFKDAIVTVDKSSSTAYMELSLTSEDSAVYYTYR---WFEDMGQGLTVTVA 133
 DB 62 QKFKDAIVTVDKSSSTAYMELSLTSEDSAVYYTYR---WFEDMGQGLTVTVA 118

RESULT 14
 O92L75 PRELIMINARY; PRT; 109 AA.
 AC O92L75.
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=BA16/C;
 RA Matkovic S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: AF206031; AAF69329.1; -
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGv; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;

Query Match 27.1%; Score 376.5; DB 11; Length 109;
 Best Local Similarity 67.9%; Pred. No. 1e-25;
 Matches 74; Conservative 10; Mismatches 20; Indels 5; Gaps 1;

QY 30 ELVPPGASVTLSCKASGYFTDYEIHWRQTPVHGLEMWIGAIIDPETGGTAVNOKRKDKAI 89
 DB 1 ELVPPGASVTLSCKASGYFTSYVHWYKQKPGQGLEWIGIYNPDGTRNEKFKGKAT 60
 QY 90 VTVDKSSSTAYMELRSLTSEDSAVYYT---RWFEEDWGQGLTVYSA 133
 DB 61 LTSDKSSSTAYMELSLTSEDSAVYYCARGDGNVGRGFDYWGQGLTVYSS 109

RESULT 15
 Q9JL81 PRELIMINARY; PRT; 114 AA.
 ID Q9JL81;
 AC Q9JL81;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RA Makiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 acetyl-glucoamine antibodies from mice with autoimmune myocarditis."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN
 CC EMBL: AF206025; AAF69323.1; -
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGv; 1.
 FT NON_TER 1
 FT NON_TER 114
 SQ SEQUENCE 114 AA; 12829 MW; 404855FDE6BA56F8 CRC64;

Query Match 26.7%; Score 371.5; DB 11; Length 114;
 Best Local Similarity 64.6%; Pred. No. 2.9e-25;
 Matches 73; Conservative 11; Mismatches 20; Indels 9; Gaps 1;

QY 30 ELVPPGASVTLSCKASGYFTDYEIHWRQTPVHGLEMWIGAIIDPETGGTAVNOKRKDKAI 89
 DB 2 QLVPPGASVTLSCKASGYFTSYVHWYKQKPGQGLEWIGIDPSDSETRLNQKFKKAT 61
 QY 90 VTVDKSSSTAYMELRSLTSEDSAVYYT---RWFEEDWGQGLTVYSA 133
 DB 62 LTVDKSSSTAYMQLSPTSEDSAVYYCARSNYGSSLYYFDYWGQGLTVYSS 114

Search completed: January 18, 2002, 01:31:24
 Job time: 451 sec

